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## OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 9.76923 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-15

Perfect score: 30

Sequence: 1 NYGMN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTCUTS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	5	US-08-783-853A-8	Sequence 8, Appli
2	30	100.0	5	US-09-344-050-8	Sequence 8, Appli
3	30	100.0	74	US-09-134-001C-3503	Sequence 3503, Ap
4	30	100.0	92	US-08-783-853A-84	Sequence 84, Appli
5	30	100.0	92	US-09-344-050-84	Sequence 84, Appli
6	30	100.0	112	US-08-783-853A-20	Sequence 20, Appli
7	30	100.0	112	US-09-344-050-20	Sequence 20, Appli
8	30	100.0	115	US-08-483-749A-24	Sequence 24, Appli
9	30	100.0	117	US-08-249-013-6	Sequence 6, Appli
10	30	100.0	117	US-08-886-863-6	Sequence 6, Appli
11	30	100.0	117	US-09-175-229-6	Sequence 6, Appli
12	30	100.0	117	PCT-US95-06764-6	Sequence 6, Appli
13	30	100.0	118	US-08-425-336-124	Sequence 124, App
14	30	100.0	118	US-08-425-336-126	Sequence 126, App
15	30	100.0	118	US-08-488-113B-124	Sequence 126, App
16	30	100.0	118	US-08-488-113B-126	Sequence 126, App
17	30	100.0	118	US-08-477-484B-124	Sequence 124, App
18	30	100.0	118	US-08-477-484B-126	Sequence 124, App
19	30	100.0	118	US-08-107-669D-28	Sequence 28, Appli
20	30	100.0	118	US-08-107-669D-29	Sequence 28, Appli
21	30	100.0	118	US-08-107-669D-66	Sequence 66, Appli
22	30	100.0	118	US-08-107-669D-67	Sequence 67, Appli
23	30	100.0	118	US-08-472-788A-28	Sequence 28, Appli
24	30	100.0	118	US-08-472-788A-29	Sequence 28, Appli
25	30	100.0	118	US-08-472-788A-88	Sequence 88, Appli
26	30	100.0	118	US-08-472-788A-89	Sequence 89, Appli
27	30	100.0	118	US-08-477-531B-28	Sequence 28, Appli

28	30	100.0	118	US-08-477-531B-29	Sequence 29, Appli
29	30	100.0	118	US-08-477-531B-66	Sequence 66, Appli
30	30	100.0	118	US-08-477-531B-67	Sequence 67, Appli
31	30	100.0	118	US-08-646-360-124	Sequence 124, App
32	30	100.0	118	US-08-646-360-126	Sequence 126, App
33	30	100.0	118	US-08-082-842A-28	Sequence 28, Appli
34	30	100.0	118	US-08-082-842A-29	Sequence 29, Appli
35	30	100.0	118	US-08-082-842A-88	Sequence 88, Appli
36	30	100.0	118	US-08-082-842A-89	Sequence 89, Appli
37	30	100.0	118	US-08-839-765-124	Sequence 124, App
38	30	100.0	118	US-08-839-765-126	Sequence 126, App
39	30	100.0	118	US-09-136-389-124	Sequence 126, App
40	30	100.0	118	US-09-136-389-126	Sequence 126, App
41	30	100.0	118	US-09-610-838-124	Sequence 124, App
42	30	100.0	118	US-09-610-838-126	Sequence 126, App
43	30	100.0	118	US-09-440-781-96	Sequence 96, Appli
44	30	100.0	118	US-09-711-485-124	Sequence 124, App
45	30	100.0	118	US-09-711-485-126	Sequence 126, App

## ALIGNMENTS

RESULT 1  
US-08-783-853A-8  
Sequence 8, Application US/08783853A  
Patent No. 6005091  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
OF THROMBOSIS  
NUMBER OF INVENTION: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,853A  
FILING DATE: 16-JAN-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,119  
FILING DATE: 24-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-783-853A-8

Query Match 100.0%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 1 NYGMN 5

RESULT 2  
US-09-344-050-8  
Sequence 8, Application US/09344050  
Patent No. 6391299

GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:

TELEX:  
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-09-344-050-8

Query Match 100.0%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 1 NYGMN 5

RESULT 3  
US-09-134-001C-3503  
Sequence 3503, Application US/09134001C  
Patent No. 6380370

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3503  
LENGTH: 74  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3503

Query Match 100.0%; Score 30; DB 3; Length 74;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 4 NYGMN 8

RESULT 4  
US-08-783-853A-84

Sequence 84, Application US/08783853A  
Patent No. 6005091  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406

COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,853A  
FILING DATE: 16-JAN-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,119  
FILING DATE: 24-OCT-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-783-853A-84

Query Match 100.0%; Score 30; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
|||  
Db 8 NYGMN 12

RESULT 5  
US-09-344-050-84  
Sequence 84, Application US/09344050  
Patent No. 6391299  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-09-344-050-84

Query Match 100.0%; Score 30; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
|||  
Db 8 NYGMN 12

RESULT 6  
US-08-783-853A-20  
Sequence 20, Application US/08783853A  
Patent No. 6005091  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Giora  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,853A  
FILING DATE: 16-JAN-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/029,119  
FILING DATE: 24-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-783-853A-20

Query Match 100.0%; Score 30; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 28 NYGMN 32

## RESULT 7

US-09-344-050-20  
Sequence 20, Application US/09344050  
Patent No. 6391299  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
APPLICANT: Church, William  
APPLICANT: Gross, Mitchell  
APPLICANT: Feuerstein, Gloria  
APPLICANT: Nichols, Andrew  
APPLICANT: Padlan, Eduardo  
APPLICANT: Patel, Arunbhai  
APPLICANT: Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
TITLE OF INVENTION: OF THROMBOSIS  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/344,050  
FILING DATE: 24-JUN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/783,853  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumelster, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50438  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5096  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-09-344-050-20

Query Match 100.0%; Score 30; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 28 NYGMN 32

RESULT 8  
US-08-483-749A-24  
Sequence 24, Application US/08483749A  
Patent No. 6054561

GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,749A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0508,008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-483-749A-24

Query Match 100.0%; Score 30; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 31 NYGMN 35

RESULT 9  
US-08-249-013-6  
Sequence 6, Application US/08249013  
Patent No. 5643754

GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Juba & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,013  
FILING DATE: 25-MAY-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: Intra  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-08-249-013-6

Query Match  
Best Local Similarity 100.0%; Score 30; DB 1; Length 117;  
Matches 5; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
Db 22 NYGMN 26

RESULT 10  
US-08-886-863-6  
Sequence 6, Application US/08886863  
Patent No. 5824321  
GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/886,863  
FILING DATE: 01-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/249,013  
FILING DATE: 25-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: Intra  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-08-886-863-6

Query Match  
Best Local Similarity 100.0%; Score 30; DB 2; Length 117;  
Matches 5; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5  
Db 22 NYGMN 26

RESULT 11  
US-09-175-229-6  
Sequence 6, Application US/09175229  
Patent No. 6309641  
GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/175,229  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/249,013  
FILING DATE: 25-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Tumarkin Ph.D., Lisa A.,  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD-3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: Intra  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
US-09-175-229-6

Query Match  
Best Local Similarity 100.0%; Score 30; DB 3; Length 117;  
Matches 5; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5

Db 22 NYGMN 26

RESULT 12  
PCT-US95-06764-6  
Sequence 6, Application PC/TUS9506764  
GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06764  
FILING DATE: 25-MAY-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.,  
REGISTRATION NUMBER: 38,347,  
REFERENCE/DOCKET NUMBER: FD3602  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: lula  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..117  
PCT-US95-06764-6

Query Match 100.0%; Score 30; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 22 NYGMN 26

RESULT 13  
US-08-425-336-124  
Sequence 124, Application US/08425336  
Patent No. 5621083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois

COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-124

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 31 NYGMN 35

RESULT 14  
US-08-425-336-126  
Sequence 126, Application US/08425336  
Patent No. 5621083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-126

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 31 NYGMN 35

RESULT 15  
US-08-488-113B-124  
Sequence 124, Application US/08488113B  
Patent No. 574580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroli, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-124

Query Match 100.0%; Score 30; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 31 NYGMN 35

Search completed: March 1, 2005, 17:46:55  
Job time: 10.7692 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 26.7692 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-15

Perfect score: 30

Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/FCI\_NEW\_PUB.pep:\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	9 US-09-965-099-8	Sequence 8, Appli
2	30	100.0	5	10 US-09-791-551-74	Sequence 74, Appli
3	30	100.0	5	13 US-10-051-852-8	Sequence 8, Appli
4	30	100.0	5	14 US-10-071-962-15	Sequence 15, Appli
5	30	100.0	5	15 US-10-430-176-8	Sequence 8, Appli
6	30	100.0	5	15 US-10-377-121-26	Sequence 26, Appli
7	30	100.0	10	9 US-09-056-160B-1	Sequence 1, Appli
8	30	100.0	10	14 US-10-234-671-1	Sequence 1, Appli
9	30	100.0	10	16 US-10-018-245A-1	Sequence 1, Appli
10	30	100.0	10	16 US-10-723-434-111	Sequence 11, App
11	30	100.0	10	16 US-10-723-434-112	Sequence 112, App
12	30	100.0	10	16 US-10-723-434-116	Sequence 116, App
13	30	100.0	10	16 US-10-723-434-122	Sequence 122, App

14	30	100.0	12	10 US-09-954-185-147	Sequence 147, App
15	30	100.0	67	14 US-10-243-130-19	Sequence 19, Appli
16	30	100.0	70	14 US-10-243-130-17	Sequence 17, Appli
17	30	100.0	70	14 US-10-243-130-18	Sequence 18, Appli
18	30	100.0	76	15 US-10-424-599-268610	Sequence 268610,
19	30	100.0	92	9 US-09-965-099-84	Sequence 84, Appli
20	30	100.0	92	13 US-10-051-852-84	Sequence 84, Appli
21	30	100.0	92	15 US-10-430-176-84	Sequence 20, Appli
22	30	100.0	112	9 US-09-965-099-20	Sequence 20, Appli
23	30	100.0	112	13 US-10-051-852-20	Sequence 20, Appli
24	30	100.0	112	15 US-10-430-176-20	Sequence 8, Appli
25	30	100.0	116	9 US-09-971-543-8	Sequence 9, Appli
26	30	100.0	116	9 US-09-971-543-9	Sequence 9, Appli
27	30	100.0	116	9 US-09-971-543-10	Sequence 10, Appli
28	30	100.0	116	14 US-10-138-727A-2	Sequence 2, Appli
29	30	100.0	116	14 US-10-138-727A-4	Sequence 4, Appli
30	30	100.0	116	14 US-10-138-727A-6	Sequence 6, Appli
31	30	100.0	116	14 US-10-138-727A-17	Sequence 17, Appli
32	30	100.0	116	14 US-10-138-727A-18	Sequence 18, Appli
33	30	100.0	116	14 US-10-138-727A-19	Sequence 19, Appli
34	30	100.0	116	14 US-10-138-727A-20	Sequence 20, Appli
35	30	100.0	116	14 US-10-138-727A-21	Sequence 21, Appli
36	30	100.0	116	14 US-10-138-727A-22	Sequence 22, Appli
37	30	100.0	116	14 US-10-138-727A-23	Sequence 23, Appli
38	30	100.0	116	14 US-10-138-727A-24	Sequence 24, Appli
39	30	100.0	116	14 US-10-138-727A-25	Sequence 25, Appli
40	30	100.0	116	14 US-10-138-727A-26	Sequence 26, Appli
41	30	100.0	116	14 US-10-310-719-30	Sequence 30, Appli
42	30	100.0	116	14 US-10-310-719-33	Sequence 33, Appli
43	30	100.0	116	15 US-10-468-170-658	Sequence 658, App
44	30	100.0	116	15 US-10-468-170-660	Sequence 660, App
45	30	100.0	116	15 US-10-468-370-662	Sequence 662, App

#### ALIGNMENTS

RESULT 1  
US-09-965-099-8  
; Sequence 8, Application US/09965099  
; Patent No. US20020136725A1  
; GENERAL INFORMATION:  
; APPLICANT: Blackburn, Michael  
; Feenstra, Giora  
; Patel, Arundhai  
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN  
; TREATMENT OF THROMBOSIS  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/965,099  
; FILING DATE: 26-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/346,487  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baumelster, Kirk  
; REGISTRATION NUMBER: 33,833  
; REFERENCE/DOCKET NUMBER: P50438-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5096

TELEFAX: <Unknown>  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-965-099-8

Query Match 100.0%; Score 30; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 1 NYGMN 5

RESULT 2  
US-09-791-551-74  
Sequence 74, Application US/09791551  
Publication No. US20030235584A1  
GENERAL INFORMATION:  
APPLICANT: KLOETZER, WILLIAM S.  
APPLICANT: HANNA, NABIL  
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES  
FILE REFERENCE: 037003/0277869  
CURRENT APPLICATION NUMBER: US/09/791,551  
CURRENT FILING DATE: 2001-02-26  
PRIOR APPLICATION NUMBER: 60/185,390  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/233,625  
PRIOR FILING DATE: 2000-09-18  
NUMBER OF SEQ ID NOS: 119  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 74  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-791-551-74

Query Match 100.0%; Score 30; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 1 NYGMN 5

RESULT 3  
US-10-051-852-8  
Sequence 8, Application US/10051852  
Publication No. US2002014641A1  
GENERAL INFORMATION:  
APPLICANT: Blackburn, Michael  
Church, William  
Grose, Mitchell  
Feuerstein, Gloria  
Nichols, Andrew  
Padlan, Eduardo  
Patel, Arunhai  
Sylvester, Daniel  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
OF THROMBOSIS  
NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/051,852

FILING DATE: 17-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/344,050

FILING DATE: 25-JUN-1999

APPLICATION NUMBER: 08/783,853

FILING DATE: 16-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833

REFERENCE/DOCKET NUMBER: P50438

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEFAX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-051-852-8

Query Match 100.0%; Score 30; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 1 NYGMN 5

RESULT 4  
US-10-071-962-15  
Sequence 15, Application US/10071962  
Publication No. US20030170237A1  
GENERAL INFORMATION:  
APPLICANT: Baufu Ni  
APPLICANT: Bill N.C. Sun  
APPLICANT: Cedilly R.Y. Sun  
TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and  
Screening Method Therefor  
FILE REFERENCE: 98-3  
CURRENT APPLICATION NUMBER: US/10/071,962  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US/09/303,155A  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: 60/083,575  
PRIOR FILING DATE: 1998-04-30  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 5

TYPE: PRT  
ORGANISM: mouse  
US-10-071-962-15

Query Match 100.0%; Score 30; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 1 NYGMN 5

RESULT 5  
US-10-430-176-8  
Sequence 8, Application US/10430176  
Publication No. US20030235587A1  
GENERAL INFORMATION:

APPLICANT: Feuerstein, Gloria Z.  
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT  
FILE REFERENCE: P50816-1  
CURRENT APPLICATION NUMBER: US/10/430,176  
PRIOR APPLICATION NUMBER: 09/817,960  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: 09/359,202  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 60/095,714  
PRIOR FILING DATE: 1998-08-07  
PRIOR APPLICATION NUMBER: 10/051,852  
PRIOR FILING DATE: 2002-01-17  
PRIOR APPLICATION NUMBER: 09/344,050  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 08/783,853  
PRIOR FILING DATE: 1997-01-06  
PRIOR APPLICATION NUMBER: 60/010,018  
PRIOR FILING DATE: 199-01-17  
PRIOR APPLICATION NUMBER: 60/029,119  
PRIOR FILING DATE: 1996-10-24  
NUMBER OF SEQ ID NOS: 111  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Home sapiens  
US-10-430-176-8

Query Match 100.0%; Score 30; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
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Db 1 NYGMN 5

RESULT 6  
US-10-377-121-26  
Sequence 26, Application US/10377121  
Publication No. US20040001825A1  
GENERAL INFORMATION:  
APPLICANT: GOVINDAM, SERENGULAM  
APPLICANT: OU, ZHENGXING  
APPLICANT: HANSEN, HANS  
APPLICANT: GOLDENBERG, DAVID  
TITLE OF INVENTION: RS7 ANTIBODIES  
FILE REFERENCE: 018733/1163  
CURRENT APPLICATION NUMBER: US/10/377,121  
CURRENT FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: 60/360,299  
PRIOR FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Mus sp.  
US-10-377-121-26

Query Match 100.0%; Score 30; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 1 NYGMN 5

RESULT 7  
US-09-056-1608-1  
Sequence 1, Application US/090561608  
Patent No. US20020032315A1  
GENERAL INFORMATION:

APPLICANT: Baca, Manuel  
APPLICANT: Wells, James A.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Lowman, Henry B.  
APPLICANT: Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,1608  
FILING DATE: 06-Apr-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/054,856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1093R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-056-1608-1

Query Match 100.0%; Score 30; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 6 NYGMN 10

RESULT 8  
US-10-234-671-1  
Sequence 1, Application US/10234671

Publication No. US20030190317A1  
GENERAL INFORMATION:  
APPLICANT: Bacq, Manuel  
Wells, James A.  
Prestea, Leonard G.  
Lowman, Henry B.  
Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/234,671  
FILING DATE: 03-Sep-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/056160  
FILING DATE: 06-APR-1998  
APPLICATION NUMBER: 60/126446  
FILING DATE: 07-APR-1997  
APPLICATION NUMBER: 60/054856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093R2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-234-671-1  
Query Match 100.0%; Score 30; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 6 NYGMN 10  
RESULT 9  
US-10-018-245A-1  
Sequence 1, Application US/10018245A  
Publication No. US20040115196A1  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, Yoshiaki  
APPLICANT: NAGAHIRA, Kazuhiro  
APPLICANT: MAKANISHI, Toshihiro  
TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement  
TITLE OF INVENTION: determining regions and genes encoding the same  
FILE REFERENCE: 46224  
CURRENT APPLICATION NUMBER: US/10/018,245A  
CURRENT FILING DATE: 2002-07-12  
PRIOR APPLICATION NUMBER: JP 117394/2000  
PRIOR FILING DATE: 2000-04-19  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1  
LENGTH: 10  
TYPE: PRT  
ORGANISM: mouse  
OTHER INFORMATION: CDR-H1 of anti-human TNF-alpha antibody  
US-10-018-245A-1  
Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 6 NYGMN 10  
RESULT 10  
US-10-723-434-111  
Sequence 111, Application US/10723434  
Publication No. US2004013357A1  
GENERAL INFORMATION:  
APPLICANT: Zhong, Pingyu  
APPLICANT: Luo, Peizhi  
APPLICANT: Wang, Kevin C.  
APPLICANT: Heleh, Mark  
APPLICANT: Li, Yan  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
FILE REFERENCE: 26050-709,501  
CURRENT APPLICATION NUMBER: US/10/723,434  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US 60/284,407  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: US 10/125,687  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 10/153,176  
PRIOR FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US 10/443,134  
PRIOR FILING DATE: 2003-05-20  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 111  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VH/CDR1  
US-10-723-434-111  
Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NYGMN 5  
Db 6 NYGMN 10  
RESULT 11  
US-10-723-434-112  
Sequence 112, Application US/10723434  
Publication No. US2004013357A1  
GENERAL INFORMATION:  
APPLICANT: Zhong, Pingyu  
APPLICANT: Luo, Peizhi  
APPLICANT: Wang, Kevin C.  
APPLICANT: Heleh, Mark  
APPLICANT: Li, Yan  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
FILE REFERENCE: 26050-709,501  
CURRENT APPLICATION NUMBER: US/10/723,434  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US 60/284,407



PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: US 10/125,687  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 10/153,176  
PRIOR FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US 10/443,134  
PRIOR FILING DATE: 2003-05-20  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 112  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VH/CDR1  
US-10-723-434-112

Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 6 NYGMN 10

RESULT 12  
US-10-723-434-116  
Sequence 116, Application US/10723434  
Publication No. US2004013357A1  
GENERAL INFORMATION:  
APPLICANT: Zhong, Pingyu  
APPLICANT: Luo, Peizhi  
APPLICANT: Wang, Kevin C.  
APPLICANT: Hsieh, Mark  
APPLICANT: Li, Yan  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
FILE REFERENCE: 26050-709, 501  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US/10/723,434  
PRIOR FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US 60/284,407  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: US 10/125,687  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 10/153,176  
PRIOR FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US 10/443,134  
PRIOR FILING DATE: 2003-05-20  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 116  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VH/CDR1  
US-10-723-434-116

Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 6 NYGMN 10

RESULT 13  
US-10-723-434-122  
Sequence 122, Application US/10723434  
Publication No. US2004013357A1  
GENERAL INFORMATION:  
APPLICANT: Zhong, Pingyu

APPLICANT: Luo, Peizhi  
APPLICANT: Wang, Kevin C.  
APPLICANT: Hsieh, Mark  
APPLICANT: Li, Yan  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR  
FILE REFERENCE: 26050-709, 501  
CURRENT FILING DATE: US/10/723,434  
PRIOR APPLICATION NUMBER: US 60/284,407  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: US 10/125,687  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 10/153,176  
PRIOR FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US 10/443,134  
PRIOR FILING DATE: 2003-05-20  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 122  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VH/CDR1  
US-10-723-434-122

Query Match 100.0%; Score 30; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 6 NYGMN 10

RESULT 14  
US-09-954-385-147  
Sequence 147, Application US/09954385  
Publication No. US20030100467A1  
GENERAL INFORMATION:  
APPLICANT: Aehele, Wolfgang  
APPLICANT: Baldwin, Toby L.  
APPLICANT: Van Gastel, Franciscus J. C.  
APPLICANT: Janssen, Giselle G.  
APPLICANT: Murray, Christopher J.  
APPLICANT: Wang, Huangling  
APPLICANT: Winietzky, Deborah S.  
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
FILE REFERENCE: GCG90  
CURRENT APPLICATION NUMBER: US/09/954,385  
CURRENT FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 433  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO: 147  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: binding peptide  
US-09-954-385-147

Query Match 100.0%; Score 30; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.3;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 6 NYGMN 10

RESULT 15  
US-10-243-130-19

; Sequence 19, Application US/10243130  
; Publication No. US20030143682A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C.  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sasse, Philip M.  
; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED  
; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY  
; FILE REFERENCE: MOR-130  
; CURRENT APPLICATION NUMBER: US/10/243,130  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/707,468  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
US-10-243-130-19

Query Match 100.0%; Score 30; DB 14; Length 67;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||  
Db 25 NYGMN 29

Search completed: March 1, 2005, 17:52:49  
Job time : 27.7692 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 6.76923 Seconds

(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-15

Perfect score: 30

Sequence: 1 NYGMN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: D1R1:\*

2: D1R2:\*

3: D1R3:\*

4: D1R4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	93	2	C24672
2	30	100.0	99	2	S26326
3	30	100.0	101	2	D24672
4	30	100.0	105	2	S24764
5	30	100.0	105	2	S24765
6	30	100.0	109	2	S26325
7	30	100.0	115	2	S19968
8	30	100.0	115	2	S19965
9	30	100.0	116	2	S69305
10	30	100.0	118	2	S19967
11	30	100.0	119	2	A53285
12	30	100.0	120	2	B42848
13	30	100.0	120	2	S12953
14	30	100.0	124	2	PH1404
15	30	100.0	146	4	S33905
16	30	100.0	146	4	B90406
17	30	100.0	175	2	S01042
18	30	100.0	726	2	AB0122
19	30	100.0	732	2	T44483
20	27	90.0	96	2	B90793
21	27	90.0	96	2	G85653
22	27	90.0	151	2	E70615
23	27	90.0	153	2	G75616
24	27	90.0	174	2	F85028
25	27	90.0	191	2	A97074
26	27	90.0	212	2	D84442
27	27	90.0	281	2	S34496
28	27	90.0	321	2	D97836
29	27	90.0	326	1	VGXK37

30	27	90.0	326	1	VGXK7H	glycoprotein VP7 p
31	27	90.0	326	1	VGXKMD	glycoprotein VP7 p
32	27	90.0	326	1	VGXKWA	glycoprotein VP7 p
33	27	90.0	329	2	T13016	hypothetical prote
34	27	90.0	338	2	T28779	hypothetical prote
35	27	90.0	340	2	T28080	hypothetical prote
36	27	90.0	344	2	H45252	p11v constant regi
37	27	90.0	373	2	A69143	galactosyl-transfe
38	27	90.0	381	2	T10341	hypothetical prote
39	27	90.0	388	2	A82903	conserved hypotnet
40	27	90.0	391	2	B83840	hypothetical prote
41	27	90.0	406	2	JC4600	isocitrate dehydro
42	27	90.0	454	2	A97147	siderophore/surfac
43	27	90.0	470	1	S14628	phosphogluconate d
44	27	90.0	560	2	S09995	nuclear factor 1-B
45	27	90.0	561	2	A31256	transcription fact

#### ALIGNMENTS

##### RESULT 1

C24672 Ig heavy chain V region (YMU-1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999

C:Accession: C24672

R:Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A:Reference number: A91022; MUID:86055722; PMID:2998759

A:Accession: C24672

A:Molecule type: DNA

A:Residues: 1-93 <WTN>

A:Cross-references: GB:X03300; NID:G52375; PIDN:CAA27039.1; PID:G773221

A:Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramet; immunoglobulin

##### Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 93;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

DB 12 NYGMN 16

##### RESULT 2

S26326 Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 17-Apr-1998

C:Accession: S26326

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26326

A:Molecule type: mRNA

A:Residues: 1-99 <STA>

A:Cross-references: EMBL:X59174

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramet; immunoglobulin

##### Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 99;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5

DB 11 NYGMN 15

## RESULT 3

D24672  
Ig heavy chain V region (VJAM3-8) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999  
C/Accession: D24672  
R/Winter, E.; Radbruch, A.; Krawinkel, U.  
EMBL J. 4, 2861-2867, 1985  
A/Reference number: A91022; MUID:86055722; PMID:2998759  
A/Accession: D24672  
A/Molecule type: DNA  
A/Residues: 1-101 <MIN>  
A/Cross-references: GB:X03301; NID:g51757; PIDN:CAA27040.1; PID:g773215  
C/Note: this sequence was determined from the differentiated gene  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 12 NYGMN 16

## RESULT 4

S24764  
Ig heavy chain V region (subgroup XI) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999  
C/Accession: S24764; S24772; S24777  
R/Klages, S.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24763  
A/Accession: S24764  
A/Molecule type: DNA  
A/Residues: 1-105 <KLA>  
A/Cross-references: EMBL:Z14999  
A/Accession: S24772  
A/Molecule type: DNA  
A/Residues: 1-105 <KLM>  
A/Cross-references: EMBL:Z15011  
R/Thomas, J.W.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24776  
A/Accession: S24777  
A/Molecule type: DNA  
A/Residues: 1-105 <THO>  
A/Cross-references: EMBL:Z15020; NID:g52616; PIDN:CAA78739.1; PID:g52617  
C/Genetics: 9/1  
A/Intons: 9/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 43 NYGMN 47

## RESULT 5

S24765  
Ig heavy chain V region (subgroup XI) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999  
C/Accession: S24765; S24773; S24778  
R/Klages, S.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24763

A/Accession: S24765  
A/Molecule type: DNA  
A/Residues: 1-105 <KLA>  
A/Cross-references: EMBL:Z15001  
A/Accession: S24773  
A/Molecule type: DNA  
A/Residues: 1-105 <KLM>  
A/Cross-references: EMBL:Z15013  
R/Thomas, J.W.  
submitted to the EMBL Data Library, August 1992  
A/Reference number: S24776  
A/Accession: S24778  
A/Molecule type: DNA  
A/Residues: 1-105 <THO>  
A/Cross-references: EMBL:Z15022; NID:g52619; PIDN:CAA78741.1; PID:g52620  
C/Genetics: 9/1  
A/Intons: 9/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 30; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 43 NYGMN 47

## RESULT 6

S26325  
Ig heavy chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S26325  
R/Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A/Title: Antibodies that are specific for a single amino acid interchange in a protein of  
A/Reference number: S26309; MUID:91341421; PMID:1908510  
A/Accession: S26325  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-109 <STA>  
A/Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:g52080; PID:g1334043  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/5-88/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYGMN 5  
|||||  
Db 21 NYGMN 25

## RESULT 7

S19968  
Ig heavy chain V region (M-T408) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S19968  
R/Weissenborn, W.; Riettmueller, G.; Weiser, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A/Description: Structural characterization of CD4 mab.  
A/Reference number: S19963  
A/Accession: S19968  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-115 <WEI>  
A/Cross-references: UNIPROT:Q921A6; EMBL:X65089  
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYGMN 5  
Db 26 NYGMN 30

## RESULT 8

S1965 Ig heavy chain V region (M-TJ21) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S1965  
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: S1963  
A:Accession: S1965  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-115 <WEI>

A:Cross-references: UNIPROT:0921A6; EMBL:X65088  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYGMN 5  
Db 24 NYGMN 28

## RESULT 9

S69305 hypothetical protein YLR280C - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L6003.10-b  
C:Species: Saccharomyces cerevisiae  
C:Date: 20-Jul-1996 #sequence\_revision 23-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: S69305  
R:Pauley, A.  
submitted to the EMBL Data Library, November 1994  
A:Description: The sequence of S. cerevisiae cosmid 8003.  
A:Reference number: S50366  
A:Accession: S69305  
A:Molecule type: DNA  
A:Residues: 1-116 <PAU>

A:Cross-references: UNIPROT:O13541; EMBL:U17243; NID:G556030; PIDN:AAB67350.1; PID:G2340  
C:Genetics:  
A:Gene: MIP8:YLR280C  
A:Cross-references: SGD:S0004270  
A:Map position: 12R  
C:Superfamily: Saccharomyces hypothetical protein YLR280C

Query Match 100.0%; Score 30; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYGMN 5  
Db 19 NYGMN 23

## RESULT 10

S1967 Ig heavy chain V region (M-T406) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S1967  
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: S1963  
A:Accession: S1967  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-118 <WEI>

A:Cross-references: UNIPROT:0921A6; EMBL:X65090  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:12-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYGMN 5  
Db 28 NYGMN 32

## RESULT 11

A53285 Ig heavy chain V and J regions, monoclonal antibody SCFT.M8.1 - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C:Accession: A53285  
R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.  
Mol. Immunol. 28, 1063-1072, 1991  
A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struc  
and their pH-reactivity profiles.  
A:Reference number: A53285; PMID:92017897; PMID:1922102  
A:Accession: A53285  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-119 <SAM>

A:Cross-references: GB:D12736; NID:G220595; PIDN:BAA02228.1; PID:G220596  
A:Note: sequence extracted from NCBI backbone (NCBI:63271, NCBI:63299)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYGMN 5  
Db 31 NYGMN 35

## RESULT 12

B42848 L6 mAb heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: B42848; S33903  
R:Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Matken, J.S.; Aruffo  
J. Biol. Chem. 267, 15352-15358, 1992  
A:Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and characte  
A:Reference number: A42848; PMID:92348410; PMID:1639794  
A:Accession: B42848  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-120 <FEU>

A:Cross-references: GB:M90690; NID:G195065; PIDN:AAA38146.1; PID:G195066  
A:Note: sequence extracted from NCBI backbone (NCBI:109960, NCBI:109961)  
A:Accession: S33903  
A:Status: preliminary

A/Molecule type: mRNA  
A/Residues: 1-120 <FE2>  
A/Cross-references: EMBL:M0691  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 31 NYGMN 35

## RESULT 13

S12953  
Ig heavy chain V region (Y13-259) - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
C/Accession: S12953  
R/Merge: T.M.; Biocca, S.; Cattaneo, A.  
FEBS Lett. 274, 193-198, 1990  
A/Title: Intracellular immunization. Cloning and intracellular expression of a monoclonal  
A/Reference number: S12953; MUID:91071431; PMID:2123805  
A/Accession: S12953  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-120 <MER>  
A/Cross-references: GB:X55179; NID:G56471; PID:CAA38964.1; PID:G56472  
A/Note: this sequence was determined from the germline gene  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 31 NYGMN 35

## RESULT 14

PH1404  
Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000  
C/Accession: PH1404; PH1406  
R/Shirasawa, T.; Miyazoe, I.; Hagihara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Tajima, T.  
J. Exp. Med. 176, 1209-1214, 1992  
A/Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in  
la virus.  
A/Reference number: PH1403; MUID:93018837; PMID:1402663  
A/Accession: PH1404  
A/Molecule type: DNA  
A/Residues: 1-124 <SH1>  
A/Accession: PH1406  
A/Molecule type: DNA  
A/Residues: 115-121 <SH2>  
C/Genetics:  
A/Intons: 16/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/35-118/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 30; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||

DB 51 NYGMN 55

RESULT 15  
S33905  
Ig heavy chain precursor V region - synthetic

C/Species: synthetic  
C/Date: 13-Jan-1995 #sequence\_revision 30-Apr-1998 #text\_change 20-Oct-2000  
C/Accession: S33905  
R/Liu, A.Y.; Robinson, R.R.; Hellstroem, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellstroem,  
Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987  
A/Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.  
A/Reference number: S33905; MUID:87204152; PMID:3106570  
A/Accession: S33905  
A/Molecule type: mRNA  
A/Residues: 1-146 <LIU>  
A/Cross-references: EMBL:M16072; NID:G195270; PID:AAA38229.1; PID:G195271

Query Match 100.0%; Score 30; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
|||||  
DB 50 NYGMN 54

Search completed: March 1, 2005, 17:44:43  
Job time : 8.76923 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 32.3846 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-15  
Perfect score: 30  
Sequence: 1 NYGMN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_prot: \*  
2: uniprot\_crembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	116	013541	013541 saccharomyc
2	30	100.0	175	1 HIS5_BUCDN	084156 buchnera ap
3	30	100.0	226	073D74	073d74 bacillus ce
4	30	100.0	244	065151	065151 bacillus li
5	30	100.0	261	06WDM4	06wdm4 acomyes igni
6	30	100.0	299	0924G6	0924g6 meriones sh
7	30	100.0	300	2 Q6WDM3	06wdm3 beaums hind
8	30	100.0	301	2 Q6WDM2	06wdm2 cricetomys
9	30	100.0	302	2 Q924G5	0924g5 gerbillurus
10	30	100.0	305	2 Q895E8	0895e8 clostridium
11	30	100.0	316	2 Q9CLC4	09clc4 pasteurella
12	30	100.0	323	2 Q8XSI6	08xsi6 ralsstonia s
13	30	100.0	326	2 Q39726	039726 human rotav
14	30	100.0	326	2 Q85033	085033 porcine rot
15	30	100.0	326	2 Q953T9	0953t9 human rotav
16	30	100.0	332	2 Q814Y5	0814y5 plasmodium
17	30	100.0	341	2 Q9N2S8	09n2s8 caenorhabdi
18	30	100.0	342	2 Q8XN57	08xn57 clostridium
19	30	100.0	387	2 Q65H58	065h58 bacillus li
20	30	100.0	398	2 Q97W83	097w83 sulfolobus
21	30	100.0	422	2 Q7URZ8	07urz8 rhodospirill
22	30	100.0	423	2 Q975B4	0975b4 sulfolobus
23	30	100.0	479	2 Q7SBB0	07sbb0 neurospora
24	30	100.0	725	2 Q6J3R6	06j3r6 escherichia
25	30	100.0	726	2 Q66619	066619 yersinia ps
26	30	100.0	726	2 Q8ZHB0	08zhb0 yersinia pe
27	30	100.0	729	2 Q8KR53	08kr53 escherichia
28	30	100.0	731	2 Q7UB05	07ub05 shigella fl
29	30	100.0	731	2 Q6DBU6	06dbu6 erwinia car
30	30	100.0	732	1 IUTR_ECOCI	PI4542 escherichia
31	30	100.0	732	2 Q93PE2	Q93pe2 shigella bo

32	30	100.0	782	2 Q6O7N8	06o7n8 escherichia
33	30	100.0	782	2 Q9XCH0	09xch0 shigella fl
34	30	100.0	783	2 Q6KD44	06kd44 escherichia
35	30	100.0	783	2 Q6U607	06u607 klebsiella
36	30	100.0	759	2 Q83PM3	083pm3 shigella fl
37	30	100.0	759	2 Q8FDW0	08fdw0 escherichia
38	30	100.0	828	2 Q8SX93	08sx93 drosophila
39	30	100.0	828	2 Q9VBX0	09vbx0 drosophila
40	30	100.0	1119	2 Q815N6	0815n6 plasmodium
41	30	100.0	1133	2 Q6CMR8	06cmr8 kluyveromyc
42	30	100.0	1480	2 Q7RN37	07rn37 plasmodium
43	30	100.0	1959	2 Q8V3G5	08v3g5 swinepox vi
44	27	90.0	36	2 Q809B8	0809b8 human rotav
45	27	90.0	36	2 Q809C3	Q809c3 human rotav

## ALIGNMENTS

RESULT 1	ID	013541	PRELIMINARY;	PRT;	116 AA.
AC	013541;				
DT	01-JAN-1998 (TRENBLREL. 05, Created)				
DT	01-JAN-1998 (TRENBLREL. 05, Last sequence update)				
DT	01-MAR-2004 (TRENBLREL. 26, Last annotation update)				
DE	Y1280CD.				
GN	Name=YLR280C;				
OS	Saccharomyces cerevisiae (Baker's yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.				
OX	NCBI_TaxID=4932;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97313267; PubMed=9169871;				
RA	Johnson M., Hillier L., Riles L., Albertmann K., Andre B., Ansgorge W.,				
RA	Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,				
RA	Entian K.D., Floeth W., Goffeau A., Hebling U., Heumann K.,				
RA	Heuss-Nietzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,				
RA	Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D.,				
RA	Muller-Auer S., Neutwich U., Obermayer B., Piravandi E., Pohl T.M.,				
RA	Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,				
RA	Scharfe M., Scherens B., Scholler P., Schwager C., Schwartz S.,				
RA	Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,				
RA	Vierdeels F., Voet M., Voickaert G., Voss H., Wambutt R., Wedler E.,				
RA	Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohnselt J.D.;				
RT	"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";				
RL	Nature 387:0-0(0).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Pauley A.;				
RL	Submitted (DEC-1994)				
RN					
RP	SEQUENCE FROM N.A.				
RA	Submitted (NOV-1994)				
RN					
RP	SEQUENCE FROM N.A.				
RA	Cherry J.M.;				
RL	Submitted (AUG-1997)				
DR	EMBL, U17243; AAB67350.1; -.				
DR	PIR, S69305; S69305.				
SQ	SEQUENCE 116 AA; 12951 MW; E3144157730E032 CRC64;				

Query Match  
Best Local Similarity 100.0%; Score 30; DB 2; Length 116;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
DB 19 NYGMN 23

RESULT 2  
HIS5\_BUCDN STANDARD: PRT: 175 AA.

AC Q84155; 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Imidazole glycerol phosphate synthase subunit hish (EC 2.4.2.-) (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hish) (IGP synthase subunit hish) (IGP synthase subunit hish) (Fragment).  
GN Name=hish;  
OS Buchnera aphidicola (subsp. Diuraphis noxia).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OX NCBI\_TaxID=118101;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Moran N.A., Mira A.;  
RT "Levels of selection on genes of mutualistic endosymbionts.";  
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: IGP catalyzes the conversion of PRPP and glutamine to IGP, AICAR and glutamate. The hish subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to hif for the synthesis of IGP and AICAR (By similarity).  
CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-ylamino)methylideneamino]-1-(5-phospho-glycerol) phosphate + 5-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-aminimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.  
CC -1- PATHWAY: Histidine biosynthesis; fitch step.  
CC -1- SUBUNIT: Heterodimer of hish and hif (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL; AF465524; AAC33042.1; -.  
DR HAMAP; MF\_00278; -; 1.  
DR InterPro; IPR000991; GATase.1.  
DR InterPro; IPR010139; IMP\_synth\_hish.  
DR Pfam; PF00117; GATase; 1.  
DR TIGRFAMs; TIGR01855; IMP\_synth\_hish; 1.  
DR PROSITE; PS00442; GATASE\_TYP\_1; 1.  
KW Glutamine amidotransferase; Histidine biosynthesis; Transferase.  
FT ACT\_SITE 78 78 By similarity.  
FT NON\_TER 175 175  
SQ SEQUENCE 175 AA; 19540 MW; E50851BA299D89C3 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 175;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 159 NYGMN 163

RESULT 3  
Q73DT4 PRELIMINARY; PRT: 226 AA.

AC Q73DT4; 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=BCF0627;  
OS Bacillus cereus (strain ATCC 10987).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=22523;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14960714; DOI=10.1093/nar/gkh258;  
RA Raako D.A., Ravel J., Oerstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.B., Toussaine N.J., Angiolini S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;  
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1.";  
RL Nucleic Acids Res. 32:977-988(2004).  
DR EMBL; AE017266; AAS39561.1; -.  
DR TIGR; BCE0627; -.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 226 AA; 25834 MW; 9CCB1655AD97185 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 226;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 218 NYGMN 222

RESULT 4  
Q65L51 PRELIMINARY; PRT: 244 AA.

AC Q65L51; 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Hypothetical protein (peptidoglycan-binding lysm, peptidoglycan-binding lysm).  
GN ORFNames=BL01953; BL01309;  
OS Bacillus licheniformis DSM 13.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=279010;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 13;  
RX PubMed=15383718;  
RA Velth B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;  
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";  
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 14580;  
RA Rey M.W., Ramaia P., Nelson B.A., Brody-Karlin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Raemussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;  
RT "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species.";  
RL Genome Biol. 5:R77-R77(2004).  
DR EMBL; AE017333; AAU40213.1; -.  
DR EMBL; CP000002; AAU22864.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 244 AA; 25925 MW; 1561DF77670470E2 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 42 NYGMN 46

RESULT 5



```

O6MDK4
ID O6MDK4 PRELIMINARY; PRT; 261 AA.
AC O6MDK4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth hormone receptor (Fragment).
OS Name=GHR;
OS Acomys Ignitus (fiery spiny mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Acomys.
OX NCBI_TaxID=60745;
RN [1]
RP SEQUENCE FROM N.A.
RA Stepan S.J., Adkins R.M., Anderson J.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY294923; AA062681.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 261
SQ SEQUENCE 261 AA; 28136 MW; F3641198C9807A3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 261;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 185 NYGMN 189

RESULT 6
Q924G6 PRELIMINARY; PRT; 299 AA.
ID Q924G6;
AC Q924G6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Meriones shawi (shaw's jird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=37435;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21219190; PubMed=11319262;
RA Adkins R.M., Gelke E.L., Rowe D., Honeycutt R.L.;
RT "Molecular phylogeny and divergence time estimates for major rodent
RT groups: evidence from multiple genes.";
RL Mol. Biol. Evol. 18:777-791(2001).
DR EMBL; AF332021; AAK71897.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 299
SQ SEQUENCE 299 AA; 32452 MW; 5E624460D1D7243E CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 299;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 198 NYGMN 202

RESULT 7
Q6WDM3 PRELIMINARY; PRT; 300 AA.
ID Q6WDM3;
AC Q6WDM3;

```

```

DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth hormone receptor (Fragment).
OS Name=GHR;
OS Beavys hindei (long-tailed pouched rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetomyinae;
OC Beavys.
OX NCBI_TaxID=70596;
RN [1]
RP SEQUENCE FROM N.A.
RA Stepan S.J., Adkins R.M., Anderson J.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY294904; AA062662.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 300
SQ SEQUENCE 300 AA; 32730 MW; 5211AC3F179BA984 CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 300;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 199 NYGMN 203

RESULT 8
Q6WDM2 PRELIMINARY; PRT; 301 AA.
ID Q6WDM2;
AC Q6WDM2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Cricetomys gambianus (Gambia rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetomyinae;
OC Cricetomys.
OX NCBI_TaxID=10085;
RN [1]
RP SEQUENCE FROM N.A.
RA Stepan S.J., Adkins R.M., Anderson J.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY294905; AA062663.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 301
SQ SEQUENCE 301 AA; 32706 MW; F599E104ECARF57D CRC64;

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 301;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5
DB 200 NYGMN 204

RESULT 9
Q924G5 PRELIMINARY; PRT; 302 AA.
ID Q924G5;
AC Q924G5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;

```

OS Gerbillurus valliianus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
OC Gerbillurus.  
OX NCBI\_TaxID=49440;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21219190; PubMed=11319262;  
RA Aakins R.M., Geilke E.L., Rowe D., Honeycutt R.L.;  
RT "Molecular phylogeny and divergence time estimates for major rodent  
RT groups: evidence from multiple genes.";  
RL Mol. Biol. Evol. 18:777-791(2001).  
DR EMBL; AF332022; AAK71898.1; -  
DR GO; GO:0004872; F:receptor activity; IEA.  
KM Receptor.  
FT NON\_TER 1 1  
SQ SEQUENCE 302 AA; 32687 MW; C08D7478B24CEAC3 CRC64;  
Query Match 100.0%; Score 30; DB 2; Length 302;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 201 NYGMN 205

RESULT 10  
Q895E8 PRELIMINARY; PRT; 305 AA.  
AC Q895E8;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Hypothetical protein CTC01328;  
GN OrderedLocustNames=CTC01328;  
OS Clostridium tetani.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium  
OX NCBI\_TaxID=1513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Massachusetts / E88;  
RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.033653100;  
RA Brueggemann H., Baumer S., Fricke W.F., Wietzer A., Liesegang H.,  
RA Decker I., Herzberg C., Martinez-Arias R., Mekl R., Henne A.,  
RA Gottschalk G.;  
RT "The genome sequence of Clostridium tetani, the causative agent of  
RT tetanus disease.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
KM EMBL; AE015940; AA035892.1; -  
DR Complete proteome.  
SQ SEQUENCE 305 AA; 34802 MW; 6AEC3E38786B98D8 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 305;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 24 NYGMN 28

RESULT 11  
Q9CLC4 PRELIMINARY; PRT; 316 AA.  
AC Q9CLC4;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE CoRA.  
GN Name=CoRA; OrderedLocustNames=PM1315;

OS Pasteurella multocida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Pasteurella.  
OX NCBI\_TaxID=747;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Pm70;  
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;  
RA May B.J., Zhang O., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;  
RT "Complete genomic sequence of Pasteurella multocida Pm70.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
RL EMBL; AE006170; AAK0339.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0015087; F:cobalt ion transporter activity; IEA.  
DR GO; GO:0015095; F:magnesium ion transporter activity; IEA.  
DR GO; GO:0006824; P:cobalt ion transport; IEA.  
DR GO; GO:0015693; P:magnesium ion transport; IEA.  
DR InterPro; IPR004488; CoRA\_transp.  
DR Pfam; PF01544; CoRA; 1.  
DR TIGRFAMs; TIGR00383; CoRA; 1.  
KM Complete proteome.  
SQ SEQUENCE 316 AA; 36422 MW; AD3EF4C4BC0ACC9 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 316;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 275 NYGMN 279

RESULT 12  
Q8XS16 PRELIMINARY; PRT; 323 AA.  
AC Q8XS16;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE PROBABLE MAGNESIUM AND COBALT TRANSPORT TRANSMEMBRANE PROTEIN.  
GN Name=RS01784; OrderedLocustNames=RS0665;  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM11000;  
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;  
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
RA Arlat M., Billault A., Brottier P., Camus J.C., Cartolico L.,  
RA Chandler M., Choisme N., Claudel-Renard C., Cumac S., Denange N.,  
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,  
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,  
RA Weisenbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
RL Nature 415:497-502(2002).  
DR EMBL; AL646080; CAD17816.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0046873; F:metal ion transporter activity; IEA.  
DR GO; GO:0030001; P:metal ion transport; IEA.  
DR Pfam; PF01544; CoRA; 1.  
KM Complete proteome.  
SQ SEQUENCE 323 AA; 36251 MW; DE264559E199DD61 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYGMN 5  
Db 275 NYGMN 279

Db 282 NYGMN 286

## RESULT 13

039726 PRELIMINARY; PRT; 326 AA.  
 AC 039726; MEDLINE=97412814; PubMed=9267457;  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DE Outer capsid protein VP7.  
 DE VP7.  
 OS Human rotavirus G3.  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus; Human rotavirus A.  
 OX NCBI\_TaxID=73036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97412814; PubMed=9267457;  
 RA Wen L., Nakayama M., Yamanishi Y., Nishio O., Fang Z.-Y., Nakagomi O.,  
 RA Araki K., Nishimura S., Hasegawa A., Muller W.E., Ushijima H.;  
 RT "Genetic variation in the VP7 gene of human rotavirus serotype 3 (G3  
 RT type) isolated in China and Japan."  
 RL Arch. Virol. 142:1481-1489(1997).  
 DR EMBL; D86274; BAA23294.1; -  
 DR GO; GO:0019028; C:Viral capsid; IEA.  
 DR InterPro; IPR001963; VP7.  
 DR Pfam; PF00434; VP7; 1.  
 DR ProDom; PD000191; VP7; 1.  
 SQ SEQUENCE 326 AA; 37318 MW; ED2375A2CBA14234 CRC64;

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 326;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5

Db 52 NYGMN 56

## RESULT 14

085033 PRELIMINARY; PRT; 326 AA.  
 AC 085033;  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE Outer capsid protein VP7.  
 DE Porcine rotavirus.  
 OS Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 OX NCBI\_TaxID=10913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ciarlet M., Luder J.E., Liprandi F.;  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; L35057; AAA47091.1; -  
 DR GO; GO:0019028; C:Viral capsid; IEA.  
 DR InterPro; IPR001963; VP7.  
 DR Pfam; PF00434; VP7; 1.  
 DR ProDom; PD000191; VP7; 1.  
 SQ SEQUENCE 326 AA; 37078 MW; 36A21B861A8F8B3E CRC64;

## Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 326;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5

Db 52 NYGMN 56

## RESULT 15

09E3T9 PRELIMINARY; PRT; 326 AA.  
 AC 09E3T9;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Outer capsid protein VP7.

DE Human rotavirus A.

OS Viruses; dsRNA viruses; Reoviridae; Rotavirus.

OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.

OX NCBI\_TaxID=10941;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=97/S48;

RA Xu S., Wang J., Hung T.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF260957; AAG5360.1; -

DR GO; GO:0019028; C:Viral capsid; IEA.

DR InterPro; IPR001963; VP7.

DR Pfam; PF00434; VP7; 1.

DR ProDom; PD000191; VP7; 1.

SQ SEQUENCE 326 AA; 37285 MW; 19479E95DAD21507 CRC64;

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 326;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGMN 5

Db 52 NYGMN 56

Search completed: March 1, 2005, 17:43:10  
 Job time : 34.3846 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 127.108 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-16

Perfect score: 101  
Sequence: 1 WINTYGTBPTAAGDFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	17	3	AAV32224
2	95	94.1	117	8	AD126496
3	94	93.1	17	5	AA680312
4	94	93.1	17	8	AD687337
5	94	93.1	19	2	AAV17490
6	94	93.1	19	2	AAV08699
7	94	93.1	19	3	AAV83642
8	94	93.1	67	7	ADH62639
9	94	93.1	70	7	ADH62638
10	94	93.1	112	7	ADC27441
11	94	93.1	112	7	ADC27449
12	94	93.1	115	4	AA884740
13	94	93.1	116	4	AA884739
14	94	93.1	116	5	AAE27830
15	94	93.1	116	5	AAE27839
16	94	93.1	116	5	AAE27837
17	94	93.1	116	5	AAE27825
18	94	93.1	116	5	AAE27826
19	94	93.1	116	5	AAE27828
20	94	93.1	116	5	AAE27832
21	94	93.1	116	5	AAE27834
22	94	93.1	116	5	ADG67541
23	94	93.1	116	5	ADG67537
24	94	93.1	116	5	ADG67543
25	94	93.1	116	5	ADG67531

26	94	93.1	116	5	ADG67533	ADG67533	KS	antibo
27	94	93.1	116	5	ADG67539	ADG67539	KS	antibo
28	94	93.1	116	5	ADG67529	ADG67529	KS	antibo
29	94	93.1	116	5	ADG67535	ADG67535	KS	antibo
30	94	93.1	116	6	AAE33431	AAE33431	Murine	KS
31	94	93.1	116	6	AAE33433	AAE33433	Murine	KS
32	94	93.1	116	6	AAE33434	AAE33434	Murine	KS
33	94	93.1	116	6	AAE33435	AAE33435	Murine	KS
34	94	93.1	116	6	AAE33414	AAE33414	Murine	KS
35	94	93.1	116	6	AAE33432	AAE33432	Murine	KS
36	94	93.1	116	6	AAE33438	AAE33438	Murine	KS
37	94	93.1	116	6	AAE33430	AAE33430	Murine	KS
38	94	93.1	116	6	AAE33437	AAE33437	Murine	KS
39	94	93.1	116	6	AAE33436	AAE33436	Murine	KS
40	94	93.1	116	6	AAO30908	AAO30908	hu-KS	ant
41	94	93.1	116	6	AAO30911	AAO30911	di-KS	ant
42	94	93.1	117	2	AAE28752	AAE28752	Heavy cha	
43	94	93.1	117	5	AAE80317	AAE80317	Anti-huma	
44	94	93.1	117	6	AAE33439	AAE33439	Murine	KS
45	94	93.1	118	2	AAE25414	AAE25414	Heavy cha	

## ALIGNMENTS

RESULT 1	AAV32224	standard; peptide; 17 AA.
ID	AAV32224	
XX	AAV32224	
AC	AAV32224	
XX	AAV32224	
DT	15-FEB-2000	(first entry)
XX		
DB	G-CSF agonist antibody mab163-93 heavy chain variable region CDR2.	
XX		
KW	Granulocyte colony stimulating factor receptor; G-CSF; mouse;	
KW	monoclonal antibody; agonist; screening; neutropenia; therapy;	
KW	complementarity determining region; CDR; mab163-93.	
XX		
OS	Mus musculus.	
XX		
PN	W09955735-A1.	
XX		
PD	04-NOV-1999.	
XX		
PF	30-APR-1999;	99WO-US009466.
XX		
PR	30-APR-1998;	98US-0083575P.
XX		
PA	(TANO-) TANOX INC.	
XX		
PI	Ni B, Sun BMC, Sun CRY;	
XX		
DR	WPI; 2000-052805/04.	
XX		
PT	Treatment of neutropenia by stimulating proliferation of neutrophilic	
XX	cell lineage progenitors.	
PS	Claim 13; Page 30; 64pp; English.	
XX		
CC	The present sequence represents complementarity determining region 2	
CC	(CDR2) of the heavy chain variable region of murine monoclonal antibody	
CC	mab163-93. This antibody is an example of an agonist molecule that	
CC	specifically binds to or interacts with human granulocyte colony	
CC	stimulating factor (G-CSF) receptor to stimulate cell proliferation and	
CC	differentiation, especially by dimerizing the receptor or activating	
CC	phosphorylation of kinases associated with the receptor. Agonist	
CC	antibodies can be used to stimulate proliferation of G-CSF-dependent	
CC	cells, e.g. to differentiate leading to a repopulation of neutrophilic	
CC	granulocyte lineage cells, especially to treat neutropenia (claimed).	
CC	They can also be used to detect human G-CSF receptor immunologically	
XX		
SO	Sequence 17 AA:	

XX  
XX  
AC  
XX  
ADS87337;

Query Match	93.1%	Score 94	DB 8	Length 17
Best Local Similarity	94.1%	Pred. No. 5.8e-07		
Matches 16	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Oy	1 WINTYTGSEPTYAGDFKG 17			
Db	1 WINTYTGSEPTYADDFKG 17			
RESULT 5				
AAIY17490				
ID	AAIY17490 standard; peptide; 19 AA.			
XX				
AC	AAIY17490;			
XX				
DT	03-AUG-1999 (first entry)			
XX				
DE	Mab 31.1 CDR sequence derived peptide COL311 H2.			
XX				
KM	Heavy chain variable region; 2CAVHCOL1; light chain variable region;			
KM	light chain consensus region; heavy chain consensus region; antibody;			
KM	anti-idiotype response; modified immunoglobulin; infectious disease;			

CC The present invention describes vaccines for generating an anti-idiotypic  
 CC response to an antigen. Vaccine (A), comprising, apart from a carrier, a  
 CC first immunoglobulin (I), comprising a variable region (V), or its  
 CC fragment that includes V, which is identical to a second immunoglobulin  
 CC (II), or its corresponding fragment, which can bind specifically to an  
 CC antigen (Ag), except for one or more amino acid (aa) substitutions in V.  
 CC These substitutions involve replacement of Cys residues involved in  
 CC disulfide bridge formation by residues that do not contain a thiol group.  
 CC (A) are used to raise an anti-idiotypic response (preferably both cellular  
 CC and humoral), particularly for treating a wide range of tumours (or  
 CC precancerous conditions) and infectious diseases (viral, bacterial,  
 CC fungal, parasitic), specifically syphilis, gonorrhea, acquired immune  
 CC deficiency syndrome, malaria, shigellosis, salmonella, hepatitis A or C,  
 CC Lyme disease, encephalitis, herpes, gram-positive or -negative bacterial  
 CC infections, or pneumococcal infections. Antibodies raised against the  
 CC vaccine may be recovered and administered to a second subject. (I) may  
 CC also be used for treating autoimmune diseases and allergy. Modifying (II)  
 CC so that it can no longer form intrachain disulfide bridges reduces  
 CC conformational constraints and results in significantly better anti-  
 CC idiotypic responses. The present sequence represents a *Wob* 31.1 CDR  
 CC sequence derived peptide from an example from the present invention.  
 CC  
 CC Sequence 19 AA:

RESULT 6	
AAV08699	
ID	AAV08699 standard; protein; 19 AA.
XX	
XX	
XX	AAV08699;
AC	
XX	
DT	10-AUG-1999 (first entry)
XX	
DE	Human colon carcinoma-associated protein antigen binding fragment 5.
XX	
KM	Immunoglobulin; immunospecific; variable domain; CDR; cancer antigen;
KM	complementarity determining region; infectious disease agent antigen;
KM	cellular receptor; infectious agent; chemotherapeutic agent; vaccine;
KM	cancer; infectious disease; autoimmune disease; rheumatoid arthritis;
KM	ulcerative colitis; psoriasis; allergy; immunoassay reagent; diagnosis;
KM	veterinary medicine; antibody; immunisation; antibody; immune tolerance;
KM	human colon cancer-associated protein antigen; cryptic expression;

KW	anti-idiotypic immune response.
XX	
OS	Homo sapiens.
XX	
PN	WO9925378-A1.
XX	
PD	27-MAY-1999.
XX	
PF	13-NOV-1998; 98WO-US024302.
XX	
PR	14-NOV-1997; 97US-0065716P.
PR	10-APR-1998; 98US-0081403P.
XX	
PA	(EURO-) EUROCELTIQUE SA.
XX	
PI	Burch RM;
XX	
DR	WPI, 1999-357555/30.
XX	
PT	Modified immunoglobulins including engineered binding site.
XX	
RS	Claim 6; Page 75; 123pp; English.

XX This invention describes a novel modified immunoglobulin (mig), or its  
CC fragment, that binds immunospecifically to one member (M1) of a binding  
CC pair comprising a variable domain (V) having at least one CDR  
CC (complementarily determining region) that contains a portion of the  
CC second member (M2) of the pair. This portion is not present in the  
CC natural CDR and M1 is a cancer antigen, infectious disease agent antigen,  
CC a cellular receptor for an infectious agent (provided the binding site is  
CC not NAMP or WNDP) or a member of a receptor-ligand pair. mig (also  
CC related molecules containing the same V region), optionally coupled to a  
CC chemotherapeutic agent, are used in therapeutic and/or prophylactic  
CC compositions, or vaccines, against cancers, infectious or autoimmune  
CC diseases (rheumatoid arthritis, ulcerative colitis or psoriasis) or  
CC allergies. They can also be used as immunoassay reagents for diagnosing  
CC these conditions. mig can be used in human or veterinary medicine. mig  
CC have higher affinity or specificity than native antibodies. Manipulation  
CC of CDR ensures binding specificity and avoids the unpredictable  
CC immunization and screening procedures currently used. It is now possible  
CC to generate antibodies against antigens that are inaccessible, by virtue  
CC of immune tolerance or cryptic expression. mig neutralize antigens  
CC directly or they induce an anti-idiotypic immune response. This sequence  
CC represents a fragment of modified immunoglobulin that immunospecifically  
CC binds to a binding pair in which the first member is the human colon  
CC carcinoma-associated protein antigen

SQ Sequence 19 AA;

```

Query Match Similarity 93.1%; Score 94; DB 2; Length 19;
Best Local Similarity 94.1%; Pred. No. 6.5e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY 1 WINTYTGSEPTYADDEKG 17
   |||||
Db 3 WINTYTGSEPTYADDEKG 19
   |||||

```

SEQUENCE	SEQUENCE	SEQUENCE
RESULT 7.		
AAy83642		
ID	AAy83642 standard; peptide; 19 AA.	
XX		
AC	AAy83642;	
XX		
DT	29-AUG-2000 (first entry)	
XX		
DE	Biotin labelled peptide derived from CDR region of Mab31.1.	
XX		
XX		
KW	Vaccine; contraceptive; antibody; monoclonal antibody; Mab;	
KW	disulphide bond; complementary determining region; CDR; reproduction;	
KW	immune response; anti-idiotype response; light chain; heavy chain;	
KW	variable region; SP-10 epitope.	
XX		

OS	Mus musculus.	
XX		
PH	Key	location/Qualifiers
FT	Modified-site	1
FT		/label= Biotinylated
XX		
PN	WO20029443-A1.	
XX		
PD	25-MAY-2000.	
XX		
PF	12-NOV-1999;	99WO-US026671.
XX		
PR	13-NOV-1998;	98US-0108325P.
XX		
PA	(EURO-) EUROCELTRIQUE SA.	
XX		
PI	Burch RM, Sackler DA;	
XX		
DR	WPI; 2000-387748/33.	
XX		
PT	Novel vaccine composition useful as contraceptive comprises first immunoglobulin capable of inducing an anti-idiotypic response and identical to second immunoglobulin having complementarity determining region.	
PT		
XX		
PS	Example 6.6; Page 40; 77pp; English.	

XX A new contraceptive vaccine is described which comprises an antibody  
CC which has at least one complementary determining region (CDR) containing  
CC a peptide fragment of a protein associated with reproductive function  
CC capable of eliciting an anti-idiotypic response. The antibody is modified  
CC such that one or more variable region cysteine residues that form  
CC intrachain disulfide bonds are substituted for amino acids lacking a  
CC sulfhydryl group and incapable of forming such bonds e.g. Alanine. The  
CC vaccine formulation is suitable for both males and females. The method is  
CC convenient, effective, does not pose health risks and is cheap. In a  
CC particular example, a modified antibody derived from the monoclonal  
CC antibody MAb31.1 which recognises an antigen on human colon carcinomas  
CC had alanine residues substituted for the cysteine residues at positions  
CC 22 and 92 of the heavy chain variable region and at positions 23 and 88  
CC of the light chain variable region. The modified variable regions were  
CC designated 2CAVHC01 and 2CAVLC01. MAb31.1, modified MAb31.1 and  
CC bivalent peptides derived from the CDR 8 of MAb31.1 were injected  
CC into mice (See AY85636-185643) in order to generate antisera against the  
CC CDR regions of MAb31.1 and the antibodies. This peptide was designated  
CC CO311H2

```
Query Match          93.1% Score 94; DB 3; Length 19;
Best Local Similarity 94.1%; Pred. No. 6-5e-07;
Matches    16; Conservative   0; Mismatches    1; Indels
QY         1 WINTYTGEPTTAAAGDFKG 17      .
           |||||
Db          3 WINTYTGEPTTAAADDFKG 19
           |||||
```

```

RESULT 8
ADH62639
ID ADH62639 standard; protein; 67 AA.
XX
XX ADH62639;
AC
XX
XX 25-MAR-2004 (first entry)
DT
XX
XX Mouse anti-IGF antibody heavy chain consensus.
DE
XX
XX Mouse; IGF; antibody; heavy chain; primer; monoclonal antibody; H8134;
KW H36.
XX
XX Synthetic.
OS
OS Mus sp.

```



XX US2003143682-A1.  
 XX 31-JUL-2003.  
 XX 13-SEP-2002; 2002US-00243130.  
 XX 07-NOV-2000; 2000US-00707468.  
 XX (NICO/) NICOLAIDES N C.  
 XX (GRAS/) GRASSO L.  
 XX (SASS/) SASS P M.  
 XX Nicolaides NC, Graess L, Sasse PM;  
 XX WPI; 2003-635957/60.  
 XX Increasing affinity of a monoclonal antibody for an antigen by  
 XX substituting amino acids within the antibody, useful for producing  
 XX altered antibodies with enhanced biochemical activity.  
 XX Example 6; SEQ ID NO 19; 30pp; English.  
 XX The invention relates to increasing affinity of a monoclonal antibody for  
 XX an antigen comprising substituting an amino acid within the variable  
 XX domain of the heavy or light chain of the monoclonal antibody with a  
 XX second amino acid having a non-polar side chain, or with a proline where  
 XX the amino acid comprises a non-polar side chain, and where the monoclonal  
 XX antibody for the antigen is increased. Also disclosed are nucleic acids,  
 XX polypeptides, vectors, host cells and transgenic animals used in the  
 XX method of the invention. The methods and compositions of the present  
 XX invention are useful for generating antibody-producing cells with  
 XX increased level of antibody production. Cellular analysis of HB134 clones  
 XX with higher Mab levels within the conditioned medium (CM) were analysed  
 XX to determine if the increased production was simply due to genetic  
 XX alterations at the Ig locus that may lead to over-expression of the  
 XX polypeptides forming the antibody or due to enhanced secretion of the  
 XX genetic alteration affecting secretory pathway mechanisms. Three HB134  
 XX clones that had increased levels of antibody within their CM were  
 XX expanded. 10000 cells were prepared for western blot analysis to assay  
 XX for intracellular steady state Ig protein levels. H36 cells were used as  
 XX standard reference and a rodent fibroblast was used as an Ig negative  
 XX control. Cells were pelleted by centrifugation and lysed directly in 300  
 XX microl of SDS lysis buffer and boiled for 5 minutes. Lysate proteins were  
 XX separated by electrophoresis on 4-12% NuPAGE gels for analysis of Ig  
 XX heavy chain. Gels were electroblotted onto Immobilon-P in 48 mM Tris  
 XX base, 40 mM glycine, 0.0375% SDS, 20% methanol and blocked at room  
 XX temperature for 1 hour in Tris-buffered saline plus 0.05% Tween-20 and 5%  
 XX condensed milk. The results showed an increased Ab production while  
 XX others had a similar steady state level as the control sample, yet had  
 XX higher levels of Ab within the CM. These data suggest a mechanism whereby  
 XX a subset of HB134 clones contained a genetic alteration that in turn  
 XX produces elevated secretion of antibody. HB134 was derived from H36 (an  
 XX anti-human IgG antibody) by introducing a dominant negative mutant form  
 XX of PMS2 (a deletion mutant lacking amino acids 134 onwards), a mismatch  
 XX repair protein. The present sequence is a consensus heavy chain variable  
 XX region from H36 and its mutant.  
 XX Sequence 67 AA:  
 XX  
 XX Query Match 93.1%; Score 94; DB 7; Length 67;  
 XX Best Local Similarity 94.1%; Pred. No. 2.4e-06;  
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYGTGPTVAGDFKG 17  
 |||||  
 DB 44 WINTYGTGPTVADDFKG 60

RESULT 9  
 ADH62638  
 ID ADH62638 standard; protein; 70 AA.

AC ADH62638;  
 XX 25-MAR-2004 (first entry)  
 XX Mouse anti-IgG antibody H36 heavy chain.  
 XX Mouse; IgG; antibody; Heavy chain; primer; monoclonal antibody; HB134;  
 XX H36.  
 XX Mus sp.  
 XX US2003143682-A1.  
 XX 31-JUL-2003.  
 XX 13-SEP-2002; 2002US-00243130.  
 XX 07-NOV-2000; 2000US-00707468.  
 XX (NICO/) NICOLAIDES N C.  
 XX (GRAS/) GRASSO L.  
 XX (SASS/) SASS P M.  
 XX Nicolaides NC, Graess L, Sasse PM;  
 XX WPI; 2003-635957/60.  
 XX Increasing affinity of a monoclonal antibody for an antigen by  
 XX substituting amino acids within the antibody, useful for producing  
 XX altered antibodies with enhanced biochemical activity.  
 XX Claim 7; SEQ ID NO 18; 30pp; English.  
 XX The invention relates to increasing affinity of a monoclonal antibody for  
 XX an antigen comprising substituting an amino acid within the variable  
 XX domain of the heavy or light chain of the monoclonal antibody with a  
 XX second amino acid having a non-polar side chain or with a proline where  
 XX the amino acid comprises a non-polar side chain, and where the monoclonal  
 XX antibody for the antigen is increased. Also disclosed are nucleic acids,  
 XX polypeptides, vectors, host cells and transgenic animals used in the  
 XX method of the invention. The methods and compositions of the present  
 XX invention are useful for generating antibody-producing cells with  
 XX increased level of antibody production. Cellular analysis of HB134 clones  
 XX with higher Mab levels within the conditioned medium (CM) were analysed  
 XX to determine if the increased production was simply due to genetic  
 XX alterations at the Ig locus that may lead to over-expression of the  
 XX polypeptides forming the antibody or due to enhanced secretion of due to a  
 XX genetic alteration affecting secretory pathway mechanisms. Three HB134  
 XX clones that had increased levels of antibody within their CM were  
 XX expanded. 10000 cells were prepared for western blot analysis to assay  
 XX for intracellular steady state Ig protein levels. H36 cells were used as  
 XX standard reference and a rodent fibroblast was used as an Ig negative  
 XX control. Cells were pelleted by centrifugation and lysed directly in 300  
 XX microl of SDS lysis buffer and boiled for 5 minutes. Lysate proteins were  
 XX separated by electrophoresis on 4-12% NuPAGE gels for analysis of Ig  
 XX heavy chain. Gels were electroblotted onto Immobilon-P in 48 mM Tris  
 XX base, 40 mM glycine, 0.0375% SDS, 20% methanol and blocked at room  
 XX temperature for 1 hour in Tris-buffered saline plus 0.05% Tween-20 and 5%  
 XX condensed milk. The results showed an increased Ab production while  
 XX others had a similar steady state level as the control sample, yet had  
 XX higher levels of Ab within the CM. These data suggest a mechanism whereby  
 XX a subset of HB134 clones contained a genetic alteration that in turn  
 XX produces elevated secretion of antibody. HB134 was derived from H36 (an  
 XX anti-human IgG antibody) by introducing a dominant negative mutant form  
 XX of PMS2 (a deletion mutant lacking amino acids 134 onwards), a mismatch  
 XX repair protein. The present sequence is the wild-type heavy chain  
 XX variable region of antibody H36.  
 XX Sequence 70 AA:  
 XX  
 XX Query Match 93.1%; Score 94; DB 7; Length 70;  
 XX Best Local Similarity 94.1%; Pred. No. 2.5e-06;  
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGEPTYAGDFKG 17  
 |||||  
 DB 47 WINTYGEPTYADDFKG 63

RESULT 10  
 ADC27441

ID ADC27441 standard; protein; 112 AA.

AC ADC27441;

DT 18-DEC-2003 (first entry)

DE TMEFP2#18 heavy chain variable region SEQ ID NO:10.

KW antibody; TMEFP2#19; TMEFP2; binding inhibitor; prostate cancer;  
 KM cytostatic; vaccine; primary prostate cancer; metastatic prostate cancer;  
 XX locally advanced prostate cancer; androgen independent prostate cancer.

OS Synthetic.

PN WO2003075855-A2.

PD 18-SEP-2003.

PF 07-MAR-2003; 2003WO-US007209.

PR 08-MAR-2002; 2002US-0362837P.

PR 27-DEC-2002; 2002US-0436812P.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

PI Bhaskar V, De la Calle A, Law D, Caras I, Ramakrishnan V;

PI Murray R, Afar D, Powers D;

DR WPI; 2003-756783/71.

DR N-PSDB; ADC27440.

PT New antibody that competitively inhibits binding of TMEFP219 to TMEFP2,  
 useful for treating prostate cancer, e.g. primary, metastatic, locally  
 advanced, or androgen independent prostate cancer.

PT Example 1; SEQ ID NO 10; 51pp; English.

XX The present invention describes an antibody (I) that competitively  
 CC inhibits binding of TMEFP2#19 to TMEFP2. Also described: (1) a  
 CC pharmaceutical composition comprising the antibody and a carrier; (2)  
 CC detecting a prostate cancer cell in a biological sample from a patient by  
 CC contacting the biological sample with the antibody; (3) inhibiting  
 CC proliferation of a prostate cancer-associated cell by contacting the cell  
 CC with the antibody; and (4) treating prostate cancer with an antibody to  
 CC TMEFP2. (I) has cytostatic activity and can be used in vaccines. The  
 CC antibody, composition and method are useful for treating prostate cancer,  
 CC e.g. primary prostate cancer, metastatic prostate cancer, locally  
 CC advanced prostate cancer, androgen independent prostate cancer, prostate  
 CC cancer that has been treated with neoadjuvant therapy, or prostate cancer  
 CC that is refractory to treatment with neoadjuvant therapy. The present  
 CC sequence is used in the exemplification of the present invention.

XX Sequence 112 AA;

Query Match 93.1%; Score 94; DB 7; Length 112;

Best Local Similarity 94.1%; Pred. No. 4e-06; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGEPTYAGDFKG 17  
 |||||  
 DB 50 WINTYGEPTYADDFKG 66

AC AAB84740;

RESULT 11  
 ADC27449

ID ADC27449 standard; protein; 112 AA.

AC ADC27449;

DT 18-DEC-2003 (first entry)

DE TMEFP2#21 heavy chain variable region SEQ ID NO:18.

KW antibody; TMEFP2#19; TMEFP2; binding inhibitor; prostate cancer;  
 KM cytostatic; vaccine; primary prostate cancer; metastatic prostate cancer;  
 XX locally advanced prostate cancer; androgen independent prostate cancer.

OS Synthetic.

PN WO2003075855-A2.

PD 18-SEP-2003.

PF 07-MAR-2003; 2003WO-US007209.

PR 08-MAR-2002; 2002US-0362837P.

PR 27-DEC-2002; 2002US-0436812P.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

PI Bhaskar V, De la Calle A, Law D, Caras I, Ramakrishnan V;

PI Murray R, Afar D, Powers D;

DR WPI; 2003-756783/71.

DR N-PSDB; ADC27448.

PT New antibody that competitively inhibits binding of TMEFP219 to TMEFP2,  
 useful for treating prostate cancer, e.g. primary, metastatic, locally  
 advanced, or androgen independent prostate cancer.

PT Example 1; SEQ ID NO 18; 51pp; English.

XX The present invention describes an antibody (I) that competitively  
 CC inhibits binding of TMEFP2#19 to TMEFP2. Also described: (1) a  
 CC pharmaceutical composition comprising the antibody and a carrier; (2)  
 CC detecting a prostate cancer cell in a biological sample from a patient by  
 CC contacting the biological sample with the antibody; (3) inhibiting  
 CC proliferation of a prostate cancer-associated cell by contacting the cell  
 CC with the antibody; and (4) treating prostate cancer with an antibody to  
 CC TMEFP2. (I) has cytostatic activity and can be used in vaccines. The  
 CC antibody, composition and method are useful for treating prostate cancer,  
 CC e.g. primary prostate cancer, metastatic prostate cancer, locally  
 CC advanced prostate cancer, androgen independent prostate cancer, prostate  
 CC cancer that has been treated with neoadjuvant therapy, or prostate cancer  
 CC that is refractory to treatment with neoadjuvant therapy. The present  
 CC sequence is used in the exemplification of the present invention.

XX Sequence 112 AA;

Query Match 93.1%; Score 94; DB 7; Length 112;

Best Local Similarity 94.1%; Pred. No. 4e-06; Mismatches 1; Indels 0; Gaps 0;

OY 1 WINTYGEPTYAGDFKG 17  
 |||||  
 DB 50 WINTYGEPTYADDFKG 66

AC AAB84740;

RESULT 12  
 AAB84740

ID AAB84740 standard; protein; 115 AA.

AC AAB84740;

DT 17-SEP-2001 (first entry)

DE Variable region of the heavy chain of murine antibody 3A2D3.

KM Heavy chain; antibody 3A2D3; polyglutamine expansion;  
 KW neurodegenerative disorder; Huntington's disease.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200151522-A1.  
 XX  
 PD 19-JUL-2001.  
 XX  
 XX 05-JAN-2001; 2001WO-US000361.  
 PF  
 XX 07-JAN-2000; 2000US-00478960.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Finkbeiner S;  
 PI  
 XX WPI; 2001-451842/48.  
 DR  
 XX  
 XX Novel antibody useful for detecting the presence of polyglutamine  
 PT expansion comprising protein in a sample, binds to the protein in a  
 PT manner that differs from the 1C2 monoclonal antibody.  
 PS  
 XX Disclosure; Page 18; 35pp; English.  
 CC The present chain represents the variable region of the heavy chain of  
 CC murine antibody 3A2D3. This antibody recognizes a protein having a  
 CC polyglutamine expansion, where the number percentage of non-glutamine  
 CC residues in the polyglutamine expansion does not exceed 10. The antibody  
 CC binds to the protein in a manner that differs from the 1C2 monoclonal  
 CC antibody. The antibodies are used to modulate intracellular binding  
 CC activity of polyglutamine expansion. The antibodies are useful for  
 CC detecting an agent capable of modulating the binding interaction between  
 CC polylglutamine expansion comprising protein in a cell and a target of the  
 CC protein. They are also useful in immunoassays that are capable of  
 CC providing the detection of disease associated polyglutamine expansion  
 CC containing proteins. The antibodies are useful for treating a host  
 CC suffering from a disease condition associated with the presence of  
 CC polyglutamine expansion containing protein, such as neurodegenerative  
 CC disorders, e.g. Huntington's disease  
 CC  
 XX  
 SQ Sequence 115 AA;  
 Query Match 93.1%; Score 94; DB 4; Length 115;  
 Best Local Similarity 94.1%; Pred. No. 4.1e-06;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 WINTYTGPTVAGDFKG 17  
 |||||  
 49 WINTYTGPTVADDFKG 65  
 Db  
 RESULT 13  
 AAB84739  
 ID AAB84739 standard; protein; 116 AA.  
 AC AAB84739;  
 XX  
 XX 17-SEP-2001 (first entry)  
 DT  
 XX  
 DE Variable region of the heavy chain of murine antibody IF11E5.  
 XX  
 KM Heavy chain; antibody IF11E5; polyglutamine expansion;  
 KW neurodegenerative disorder; Huntington's disease.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200151522-A1.  
 XX  
 PD 19-JUL-2001.  
 PF  
 XX 05-JAN-2001; 2001WO-US000361.  
 PR  
 XX

PR 07-JAN-2000; 2000US-00478960.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Finkbeiner S;  
 PI  
 XX WPI; 2001-451842/48.  
 DR  
 XX  
 XX Novel antibody useful for detecting the presence of polyglutamine  
 PT expansion comprising protein in a sample, binds to the protein in a  
 PT manner that differs from the 1C2 monoclonal antibody.  
 PS  
 XX Disclosure; Page 18; 35pp; English.  
 CC The present chain represents the variable region of the heavy chain of  
 CC murine antibody IF11E5. This antibody recognizes a protein having a  
 CC polyglutamine expansion, where the number percentage of non-glutamine  
 CC residues in the polyglutamine expansion does not exceed 10. The antibody  
 CC binds to the protein in a manner that differs from the 1C2 monoclonal  
 CC antibody. The antibodies are used to modulate intracellular binding  
 CC activity of polyglutamine expansion. The antibodies are useful for  
 CC detecting an agent capable of modulating the binding interaction between  
 CC polylglutamine expansion comprising protein in a cell and a target of the  
 CC protein. They are also useful in immunoassays that are capable of  
 CC providing the detection of disease associated polyglutamine expansion  
 CC containing proteins. The antibodies are useful for treating a host  
 CC suffering from a disease condition associated with the presence of  
 CC polyglutamine expansion containing protein, such as neurodegenerative  
 CC disorders, e.g. Huntington's disease  
 CC  
 XX  
 SQ Sequence 116 AA;  
 Query Match 93.1%; Score 94; DB 4; Length 116;  
 Best Local Similarity 94.1%; Pred. No. 4.2e-06;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 WINTYTGPTVAGDFKG 17  
 |||||  
 49 WINTYTGPTVADDFKG 65  
 Db  
 RESULT 14  
 AAE27830  
 ID AAE27830 standard; protein; 116 AA.  
 AC AAE27830;  
 XX  
 XX 13-DEC-2002 (first entry)  
 DT  
 XX  
 DE Mouse KS de-immunised VH2 modified epitope.  
 XX  
 KM Mouse; fusion protein; immunological; major histocompatibility complex;  
 KW MHC; gastric upset; nausea; epitope; KS antibody.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200266514-A2.  
 XX  
 PD 29-AUG-2002.  
 DT  
 XX  
 DE 18-FEB-2002; 2002WO-EP001690.  
 PF  
 XX 19-FEB-2001; 2001EP-00103955.  
 PR  
 XX 05-APR-2001; 2001EP-00108291.  
 PA  
 XX (MERE ) MERCK PATENT GMBH.  
 PI  
 XX Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;  
 PI Hanlon M, Watkins J, Baker M, Way JC;  
 XX WPI; 2002-667054/71.  
 DR  
 XX New modified fusion protein with reduced immunogenicity, useful for

PT combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target polypeptide.

XX Example 19; Page 75; 92pp; English.

XX The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favorable properties of a composition or in creating new proteins of a composition which elicits biological or pharmacological efficacy without having undesirable physiological effects such as nausea or gastric upset. The present sequence is mouse KS antibody modified epitope. This sequence is used in the exemplification of the invention

CC Sequence 116 AA;

Query Match 93.1%; Score 94; DB 5; Length 116;  
Best Local Similarity 94.1%; Pred. No. 4.2e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTVAGDFKG 17  
|||  
50 WINTYTGPTVADDFKG 66

Db

RESULT 15  
AAE27839  
ID AAE27839 standard; protein; 116 AA.

AC AAE27839;

DT 13-DEC-2002 (first entry)

XX Mouse KS VH protein #2.

XX Mouse; fusion protein; immunological; major histocompatibility complex; MHC; gastric upset; nausea; KS antibody.

OS Mus sp.

XX WO200266514-A2.

PN 29-AUG-2002.

PD 18-FEB-2002; 2002WO-EP001690.

XX 19-FEB-2001; 2001EP-00103955.

PR 05-APR-2001; 2001EP-00108291.

XX (MERE ) MERCK PATENT GMBH.

XX Gillies S, Carr FU, Jones T, Carter G, Hamilton A, Williams S;  
PI Hanlon M, Watkins J, Baker M, Way JC;  
XX WPI; 2002-667054/71.

DR

XX New modified fusion protein with reduced immunogenicity, useful for combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target polypeptide.

PT Example 19; Page 76; 92pp; English.

XX The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in

CC combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological efficacy without having undesirable physiological effects such as nausea or gastric upset. The present sequence is mouse KS antibody protein. This sequence is used in the exemplification of the invention

CC Sequence 116 AA;

Query Match 93.1%; Score 94; DB 5; Length 116;  
Best Local Similarity 94.1%; Pred. No. 4.2e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGPTVAGDFKG 17  
|||  
50 WINTYTGPTVADDFKG 66

Db

Search completed: March 1, 2005, 17:36:03  
Job time : 128.108 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 33.2154 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-16

Perfect score: 101

Sequence: 1 WINTYTGEPYAGDPFG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PC/US.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	90.1	160	4	US-09-318-786-35
2	91	90.1	252	3	US-08-279-772A-6
3	91	90.1	252	3	US-08-902-486-9
4	89	88.1	118	1	US-08-425-336-124
5	89	88.1	118	1	US-08-488-113B-124
6	89	88.1	118	1	US-08-477-484B-124
7	89	88.1	118	1	US-08-107-669D-28
8	89	88.1	118	1	US-08-107-669D-29
9	89	88.1	118	1	US-08-107-669D-66
10	89	88.1	118	1	US-08-472-788A-28
11	89	88.1	118	1	US-08-472-788A-29
12	89	88.1	118	1	US-08-472-788A-88
13	89	88.1	118	2	US-08-477-531B-28
14	89	88.1	118	2	US-08-477-531B-29
15	89	88.1	118	2	US-08-477-531B-66
16	89	88.1	118	2	US-08-646-360-124
17	89	88.1	118	2	US-08-082-842A-28
18	89	88.1	118	2	US-08-082-842A-29
19	89	88.1	118	2	US-08-082-842A-88
20	89	88.1	118	3	US-08-839-765-124
21	89	88.1	118	3	US-09-136-389-124
22	89	88.1	118	3	US-09-610-838-124
23	89	88.1	118	4	US-09-440-781-96
24	89	88.1	118	4	US-09-440-781-97
25	89	88.1	118	4	US-09-711-485-124
26	89	88.1	121	4	US-09-440-781-98
27	89	88.1	121	4	US-09-440-781-99

28	89	88.1	491	4	US-10-011-125A-2	Sequence 2, Appl
29	86	85.1	140	3	US-08-569-147-76	Sequence 76, Appl
30	86	85.1	140	3	US-08-569-147-82	Sequence 82, Appl
31	86	85.1	365	3	US-08-875-811-53	Sequence 53, Appl
32	86	85.1	366	3	US-08-875-811-55	Sequence 55, Appl
33	85	84.2	136	3	US-09-184-658-32	Sequence 32, Appl
34	85	84.2	136	4	US-09-504-262D-32	Sequence 32, Appl
35	85	84.2	259	4	US-09-419-788-115	Sequence 115, Appl
36	85	84.2	278	3	US-09-184-658-47	Sequence 47, Appl
37	85	84.2	278	4	US-09-504-262D-47	Sequence 47, Appl
38	85	84.2	284	3	US-09-184-658-40	Sequence 40, Appl
39	85	84.2	284	4	US-09-504-262D-40	Sequence 40, Appl
40	84	83.2	119	4	US-09-232-280-50	Sequence 50, Appl
41	83	82.2	118	1	US-08-425-336-126	Sequence 126, App
42	83	82.2	118	1	US-08-488-113B-126	Sequence 126, App
43	83	82.2	118	1	US-08-477-484B-126	Sequence 126, App
44	83	82.2	118	1	US-08-107-669D-67	Sequence 67, Appl
45	83	82.2	118	1	US-08-472-788A-89	Sequence 89, Appl

## ALIGNMENTS

RESULT 1  
US-09-318-786-35  
Sequence 35, Application US/09318786  
Patent No. 6472147  
GENERAL INFORMATION:  
APPLICANT: Janda, Kim D  
APPLICANT: Wirsching, Peter  
APPLICANT: Lerner, Richard A  
APPLICANT: Gao, Changshou  
TITLE OF INVENTION: METHODS FOR DISPLAY OF HETEROLOGOUS PROTEINS ON  
TITLE OF INVENTION: FILAMENTOUS PHAGE USING PYL AND PLX, COMPOSITIONS,  
FILE REFERENCE: TSR0305  
CURRENT APPLICATION NUMBER: US/09/318,786  
CURRENT FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 35  
LENGTH: 160  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: fusion  
US-09-318-786-35  
Query Match  
Best Local Similarity 90.1%; Score 91; DB 4; Length 160;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
CY 1 WINTYTGEPYAGDPFG 17  
DB 52 WINTYTGEPYAGDPFG 68  
RESULT 2  
US-08-279-772A-6  
Sequence 6, Application US/08279772A  
Patent No. 6080560  
GENERAL INFORMATION:  
APPLICANT: Russell, David R  
APPLICANT: Fuller, James T  
TITLE OF INVENTION: Method for Producing Antibodies in Plant  
TITLE OF INVENTION: Cells  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESS: Quarles and Brady  
STREET: PO Box 2113  
CITY: Madison  
STATE: WI

COUNTRY: United States of America  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/279,772A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 11-229-9097-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-279-772A-6

Query Match 90.1%; Score 91; DB 3; Length 252;  
Best Local Similarity 88.2%; Pred. No. 4.7e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
|||||:|||||  
Db 180 WINTYGTQPTYADDFKG 196

RESULT 3  
US-08-902-486-9  
Sequence 9, Application US/08902486  
Patent No. 6140075  
GENERAL INFORMATION:  
APPLICANT: Russel, David R.  
APPLICANT: Fuller, James T.  
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND  
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,486  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 670513.90261  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-902-486-9

Query Match 90.1%; Score 91; DB 3; Length 252;  
Best Local Similarity 88.2%; Pred. No. 4.7e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
|||||:|||||  
Db 180 WINTYGTQPTYADDFKG 196

RESULT 4  
US-08-425-336-124  
Sequence 124, Application US/08425336  
Patent No. 5621083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studilka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-124

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
|||||:|||||  
Db 50 WINTYGEPTYADDFKG 66

APPLICANT: Bettel, Marc D.	
APPLICANT: Carroll, Stephen F.	
APPLICANT: Studnicka, Gary M.	
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating	
TITLE OF INVENTION: Proteins	
NUMBER OF SEQUENCES: 169	
CORRESPONDENCE ADDRESS:	
ADDRESSER: McAndrews, Held & Malloy, Ltd.	
STREET: 500 West Madison Street, 34th floor	
CITY: Chicago	
STATE: Illinois	
COUNTRY: USA	
ZIP: 60661	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: Patent In Release #1.0, Version #1.25	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/477,484B	
FILING DATE: 07-JUN-1995	
CLASSIFICATION: 530	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US 08/425,336	
FILING DATE: 18-APR-1995	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US 08/064,691	
FILING DATE: 12-MAY-1993	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US 07/988,430	
FILING DATE: 09-DEC-1992	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US 07/901,707	
FILING DATE: 19-JUN-1992	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US 07/787,567	
FILING DATE: 04-NOV-1991	
ATTORNEY/AGENT INFORMATION:	
NAME: McNicholas, Janet M.	
REGISTRATION NUMBER: 32,918	
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 312/707-8889	
TELEFAX: 312/707-9155	
TELEX: 650 388-1248	
INFORMATION FOR SEQ ID NO: 124:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 118 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: protein	
US-08-477-484B-124	
Query Match	88.1%; Score 89; DB 1; Length 118;
Best Local Similarity	88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY 1 WINTYGEPTYAGDFKG 17	
:	
Db 50 WINTHGEPTYADDFKG 66	
RESULT 7	
US-08-107-669D-28	
Sequence 28, Application US/08107669D	
Patent No. 5766886	
GENERAL INFORMATION:	
APPLICANT: Studnicka, Gary M.	
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)	
NUMBER OF SEQUENCES: 67	
CORRESPONDENCE ADDRESS:	
ADDRESSER: Steine, Kessler, Goldstein and Fox P.L.L.C.	

STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,669D  
CLASSIFICATION: 424  
FILING DATE: 13-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2540  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-28

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17  
DB 50 WINTHGEPTVADDFKG 66

RESULT 8  
US-08-107-669D-29  
Sequence 29, Application US/08107669D  
Patent No. 5766886  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,669D  
CLASSIFICATION: 424  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2540  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-29

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17  
DB 50 WINTHGEPTVADDFKG 66

RESULT 9  
US-08-107-669D-66  
Sequence 66, Application US/08107669D  
Patent No. 5766886  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,669D  
CLASSIFICATION: 424  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-669D-66

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



Qy 1 WINTYGEPTYAGDFKG 17  
||||:|||||  
Db 50 WINTHGEPTYADDFKG 66

## RESULT 10

US-08-472-788A-28  
Sequence 28, Application US/08472788A  
Patent No. 5770196  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,788A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-788A-28

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYAGDFKG 17  
||||:|||||  
Db 50 WINTHGEPTYADDFKG 66

## RESULT 11

US-08-472-788A-29  
Sequence 29, Application US/08472788A  
Patent No. 5770196  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,788A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-788A-29

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYAGDFKG 17  
||||:|||||  
Db 50 WINTHGEPTYADDFKG 66

## RESULT 12

US-08-472-788A-88  
Sequence 88, Application US/08472788A  
Patent No. 5770196  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,788A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-789A-88

Query Match 88.1%; Score 89; DB 1; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTHTGEPYADDFKG 17  
|||||  
DB 50 WINTHTGEPYADDFKG 66

RESULT 13  
US-08-477-531B-28  
Sequence 28, Application US/08477531B  
Patent No. 5821123  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,531B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 436  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-531B-28

Query Match 88.1%; Score 89; DB 2; Length 118;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTHTGEPYADDFKG 17  
|||||  
DB 50 WINTHTGEPYADDFKG 66

RESULT 14  
US-08-477-531B-29  
Sequence 29, Application US/08477531B  
Patent No. 5821123  
GENERAL INFORMATION:  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,531B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600

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RESULT 15
US-08-477-531B-66
; Sequence 66, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbalà
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-531B-66

Query Match      88.1%; Score 89; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 WINTYTGSEPTYAGDFKG 17
      |||:|||||
Db      50 WINTYTGSEPTYADDFKG 66

Search completed: March 1, 2005, 17:46:55
Job time : 33.2154 secs
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 91.0154 Seconds

(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-16

Perfect score: 101

Sequence: 1 WINTYGEPTAAGDFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	17	US-10-071-962-16	Sequence 16, Appl
2	94	93.1	17	US-09-791-551-86	Sequence 86, Appl
3	94	93.1	17	US-10-018-245A-2	Sequence 2, Appl1
4	94	93.1	67	US-10-243-130-19	Sequence 19, Appl
5	94	93.1	70	US-10-243-130-17	Sequence 17, Appl
6	94	93.1	14	US-10-243-130-18	Sequence 18, Appl
7	94	93.1	112	US-10-383-447-10	Sequence 10, Appl
8	94	93.1	112	US-10-383-447-18	Sequence 18, Appl
9	94	93.1	116	US-10-138-727A-2	Sequence 2, Appl1
10	94	93.1	116	US-10-138-727A-18	Sequence 18, Appl
11	94	93.1	116	US-10-138-727A-19	Sequence 19, Appl
12	94	93.1	116	US-10-138-727A-20	Sequence 20, Appl
13	94	93.1	116	US-10-138-727A-21	Sequence 21, Appl

14	94	93.1	116	US-10-138-727A-22	Sequence 22, Appl
15	94	93.1	116	US-10-138-727A-23	Sequence 23, Appl
16	94	93.1	116	US-10-138-727A-24	Sequence 24, Appl
17	94	93.1	116	US-10-138-727A-25	Sequence 25, Appl
18	94	93.1	116	US-10-138-727A-26	Sequence 26, Appl
19	94	93.1	116	US-10-310-719-30	Sequence 30, Appl
20	94	93.1	116	US-10-310-719-33	Sequence 33, Appl
21	94	93.1	116	US-10-468-370-658	Sequence 658, Appl
22	94	93.1	116	US-10-468-370-660	Sequence 660, Appl
23	94	93.1	116	US-10-468-370-662	Sequence 662, Appl
24	94	93.1	116	US-10-468-370-664	Sequence 664, Appl
25	94	93.1	116	US-10-468-370-666	Sequence 666, Appl
26	94	93.1	116	US-10-468-370-668	Sequence 668, Appl
27	94	93.1	116	US-10-468-370-670	Sequence 670, Appl
28	94	93.1	116	US-10-468-370-672	Sequence 672, Appl
29	94	93.1	116	US-10-468-370-674	Sequence 674, Appl
30	94	93.1	116	US-10-468-370-676	Sequence 676, Appl
31	94	93.1	116	US-10-468-370-678	Sequence 678, Appl
32	94	93.1	116	US-10-468-370-680	Sequence 680, Appl
33	94	93.1	116	US-10-468-370-682	Sequence 682, Appl
34	94	93.1	116	US-10-468-370-684	Sequence 684, Appl
35	94	93.1	116	US-10-468-370-686	Sequence 686, Appl
36	94	93.1	116	US-10-468-370-688	Sequence 688, Appl
37	94	93.1	117	US-10-422-049-20	Sequence 20, Appl
38	94	93.1	117	US-10-422-049-23	Sequence 23, Appl
39	94	93.1	118	US-10-422-049-19	Sequence 19, Appl
40	94	93.1	119	US-10-269-010-1	Sequence 1, Appl1
41	94	93.1	119	US-10-268-883-3	Sequence 3, Appl1
42	94	93.1	138	US-10-268-883-2	Sequence 2, Appl1
43	94	93.1	579	US-09-791-551-113	Sequence 113, Appl
44	94	93.1	579	US-10-138-727A-41	Sequence 41, Appl
45	94	93.1	579	US-10-310-719-32	Sequence 32, Appl

## ALIGNMENTS

RESULT 1  
US-10-071-962-16  
Sequence 16, Application US/10071962  
Publication No. US20030170237A1  
GENERAL INFORMATION:  
APPLICANT: Baitu N.  
APPLICANT: Bill N.C. Sun  
TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and  
TITLE OF INVENTION: Screening Method Therefor  
FILE REFERENCE: 98-3  
CURRENT APPLICATION NUMBER: US/10/071,962  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US/09/303,155A  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: 60/083,575  
PRIOR FILING DATE: 1998-04-30  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 17  
TYPE: PRT  
ORGANISM: mouse  
US-10-071-962-16

Query Match 100.0%; Score 101, DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1,1e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGEPTAAGDFKG 17  
DB 1 WINTYGEPTAAGDFKG 17

RESULT 2  
US-09-791-551-86

; Sequence 86, Application US/09791551  
; Publication No. US20030235584A1  
; GENERAL INFORMATION:  
; APPLICANT: KLOETZER, WILLIAM S.  
; APPLICANT: HANNA, NABIL  
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES  
; FILE REFERENCE: 037003/0277869  
; CURRENT APPLICATION NUMBER: US/09/791,551  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/185,390  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/233,625  
; PRIOR FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 86  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-791-551-86

Query Match 93.1%; Score 94; DB 10; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
Db 1 WINTYGEPTYADDFKG 17

RESULT 3  
US-10-018-245A-2  
; Sequence 2, Application US/10018245A  
; Publication No. US20040115196A1  
; GENERAL INFORMATION:  
; APPLICANT: FUKUDA, Yoshiaki  
; APPLICANT: NAGAHIRA, Kazuhiro  
; APPLICANT: NAKAMISHI, Toshihiro  
; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement  
; TITLE OF INVENTION: determining regions and genes encoding the same  
; FILE REFERENCE: 46224  
; CURRENT APPLICATION NUMBER: US/10/018,245A  
; CURRENT FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: JP 117394/2000  
; PRIOR FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: mouse  
; FEATURE:  
; OTHER INFORMATION: CDR-H2 of anti-human TNF-alpha antibody  
US-10-018-245A-2

Query Match 93.1%; Score 94; DB 16; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.3e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
Db 1 WINTYGEPTYADDFKG 17

RESULT 4  
US-10-243-130-19  
; Sequence 19, Application US/10243130  
; Publication No. US20030143682A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C.  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sasse, Philip M.  
; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED

; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY  
; FILE REFERENCE: MOR-130  
; CURRENT APPLICATION NUMBER: US/10/243,130  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/707,468  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
US-10-243-130-19

Query Match 93.1%; Score 94; DB 14; Length 67;  
Best Local Similarity 94.1%; Pred. No. 5.4e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
Db 44 WINTYGEPTYADDFKG 60

RESULT 5  
US-10-243-130-17  
; Sequence 17, Application US/10243130  
; Publication No. US20030143682A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C.  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sasse, Philip M.  
; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED  
; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY  
; FILE REFERENCE: MOR-130  
; CURRENT APPLICATION NUMBER: US/10/243,130  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/707,468  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-243-130-17

Query Match 93.1%; Score 94; DB 14; Length 70;  
Best Local Similarity 94.1%; Pred. No. 5.7e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
Db 47 WINTYGEPTYADDFKG 63

RESULT 6  
US-10-243-130-18  
; Sequence 18, Application US/10243130  
; Publication No. US20030143682A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolaides, Nicholas C.  
; APPLICANT: Grasso, Luigi  
; APPLICANT: Sasse, Philip M.  
; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED  
; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY  
; FILE REFERENCE: MOR-130  
; CURRENT APPLICATION NUMBER: US/10/243,130  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/707,468  
; PRIOR FILING DATE: 2000-11-07  
; NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.2  
SEQ ID NO 18  
LENGTH: 70  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-243-130-18

Query Match 93.1%; Score 94; DB 14; Length 70;  
Best Local Similarity 94.1%; Pred. No. 5.7e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
Db 47 WINTYGEPTYADDFKG 63

RESULT 7  
US-10-383-447-10

Sequence 10, Application US/10383447  
Publication No. US20040096392A1  
GENERAL INFORMATION:

APPLICANT: Bhaskar, Vinay  
APPLICANT: de la Calle, Agustín  
APPLICANT: Law, Debbie  
APPLICANT: Ramakrishnan, Vanitha  
APPLICANT: Murray, Richard  
APPLICANT: Afari, Daniel  
APPLICANT: Powers, David  
TITLE OF INVENTION: Antibodies Against Cancer Antigen TMBF2 and Uses Thereof  
FILE REFERENCE: 05882.0138.NPUS00  
CURRENT APPLICATION NUMBER: US/10/383,447  
CURRENT FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: US 60/362,837  
PRIOR FILING DATE: 2002-03-08  
PRIOR APPLICATION NUMBER: US 60/463,812  
PRIOR FILING DATE: 2002-12-27  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 10  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Heavy chain variable region  
US-10-383-447-10

Query Match 93.1%; Score 94; DB 15; Length 112;

Best Local Similarity 94.1%; Pred. No. 9.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
Db 50 WINTYGEPTYADDFKG 66

RESULT 8  
US-10-383-447-18

Sequence 18, Application US/10383447  
Publication No. US20040096392A1  
GENERAL INFORMATION:

APPLICANT: Bhaskar, Vinay  
APPLICANT: de la Calle, Agustín  
APPLICANT: Law, Debbie  
APPLICANT: Caras, Ingrid  
APPLICANT: Ramakrishnan, Vanitha  
APPLICANT: Murray, Richard  
APPLICANT: Afari, Daniel  
APPLICANT: Powers, David  
TITLE OF INVENTION: Antibodies Against Cancer Antigen TMBF2 and Uses Thereof  
FILE REFERENCE: 05882.0138.NPUS00  
CURRENT APPLICATION NUMBER: US/10/383,447  
CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US 60/362,837  
PRIOR FILING DATE: 2002-03-08  
PRIOR APPLICATION NUMBER: US 60/463,812  
PRIOR FILING DATE: 2002-12-27  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 18  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Heavy chain variable region  
US-10-383-447-18

Query Match 93.1%; Score 94; DB 15; Length 112;  
Best Local Similarity 94.1%; Pred. No. 9.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
Db 50 WINTYGEPTYADDFKG 66

RESULT 9  
US-10-138-727A-2

Sequence 2, Application US/10138727A  
Publication No. US20030157054A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Susan  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/10/138,727A  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS VH mouse  
US-10-138-727A-2

Query Match 93.1%; Score 94; DB 14; Length 116;

Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
Db 50 WINTYGEPTYADDFKG 66

RESULT 10  
US-10-138-727A-18

Sequence 18, Application US/10138727A  
Publication No. US20030157054A1  
GENERAL INFORMATION:

APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Susan  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/10/138,727A  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 18

LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: VH7 heavy chain  
US-10-138-727A-18

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
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Db 50 WINTYTGEPYADDFKG 66

RESULT 11  
US-10-138-727A-19  
Sequence 19, Application US/10138727A  
Publication No. US20030157054A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/10/138,727A  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 19  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: VH2.5 heavy chain  
US-10-138-727A-19

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||||  
Db 50 WINTYTGEPYADDFKG 66

RESULT 12  
US-10-138-727A-20  
Sequence 20, Application US/10138727A  
Publication No. US20030157054A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Qian, Susan  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/10/138,727A  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 20  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: KS VH veneered  
US-10-138-727A-20

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||||  
Db 50 WINTYTGEPYADDFKG 66

RESULT 13  
US-10-138-727A-21  
Sequence 21, Application US/10138727A  
Publication No. US20030157054A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/10/138,727A  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 21  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: KS de-immunized VH1  
US-10-138-727A-21

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||||  
Db 50 WINTYTGEPYADDFKG 66

RESULT 14  
US-10-138-727A-22  
Sequence 22, Application US/10138727A  
Publication No. US20030157054A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/10/138,727A  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 22  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: KS de-immunized VH2  
US-10-138-727A-22

Query Match 93.1%; Score 94; DB 14; Length 116;  
Best Local Similarity 94.1%; Pred. No. 9.5e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17  
|||||  
Db 50 WINTYTGEPYADDFKG 66



## RESULT 15

US-10-138-727A-23

; Sequence 23, Application US/10138727A  
; Publication No. US20030157054A1

; GENERAL INFORMATION:

; APPLICANT: Gillies, Stephen

; APPLICANT: Lo, Kin-Ming

; APPLICANT: Qian, Susan

; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

; FILE REFERENCE: LEX-019

; CURRENT APPLICATION NUMBER: US/10/138,727A

; CURRENT FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US 60/288,564

; PRIOR FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 23

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: KS de-immunized VH3

US-10-138-727A-23

## Query Match

Best Local Similarity 93.1%; Score 94; DB 14; Length 116;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYTGEPYAGDFKG 17

Db 50 WINTYTGEPYADDFKG 66

Search completed: March 1, 2005, 17:52:49  
Job time : 91.0154 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 23.0154 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-16

Perfect score: 101  
Sequence: 1 WINTYTGEPYAGDFKG 17

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	93.1	101	2 D24672	Ig heavy chain V r
2	94	93.1	105	2 S24764	Ig heavy chain V r
3	94	93.1	105	2 S24765	Ig heavy chain V r
4	94	93.1	109	2 S26325	Ig heavy chain V r
5	94	93.1	118	2 S19967	Ig heavy chain V r
6	94	93.1	119	2 A53285	Ig heavy chain V a
7	94	93.1	124	2 PH1404	Ig heavy chain V r
8	91	90.1	115	2 S19968	Ig heavy chain V r
9	91	90.1	120	2 B42848	Ig heavy chain V r
10	91	90.1	146	4 S33905	Ig heavy chain pre
11	90	89.1	102	2 C32530	Ig heavy chain V r
12	85	84.2	105	2 S24766	Ig heavy chain V r
13	84	83.2	118	2 A32530	Ig heavy chain V r
14	83	82.2	114	2 D32967	Ig heavy chain V r
15	83	82.2	114	2 C32967	Ig heavy chain V r
16	83	82.2	117	2 S32187	Ig heavy chain V r
17	83	82.2	117	2 S32190	Ig heavy chain V r
18	82	81.2	115	2 S19965	Ig heavy chain V r
19	82	81.2	136	2 S35759	Ig heavy chain V r
20	81	80.2	119	2 B32530	Ig heavy chain V r
21	80	79.2	93	2 C24672	Ig heavy chain V r
22	80	79.2	99	2 S26326	Ig heavy chain V r
23	79.5	78.7	119	2 H45722	anti-glycoprotein
24	79	78.2	113	2 B36259	Ig heavy chain V r
25	79	78.2	114	2 P40256	Ig heavy chain V r
26	79	78.2	120	2 S19963	Ig heavy chain V r
27	79	78.2	139	2 PH1225	Ig heavy chain pre
28	73	72.3	120	2 S26789	Ig heavy chain V r
29	71	70.3	98	2 S46460	Ig heavy chain V r

30	71	70.3	118	2 S37204	Ig heavy chain V r
31	66	65.3	98	2 A49051	Ig heavy chain V7
32	66	65.3	105	2 S24763	Ig heavy chain V r
33	66	65.3	117	2 S18554	Ig heavy chain V r
34	66	65.3	131	2 S26792	Ig heavy chain V r
35	62	61.4	142	2 S19245	Ig heavy chain pre
36	61	60.4	98	2 H34964	Ig heavy chain V-I
37	58	57.4	114	2 S21916	Ig heavy chain V r
38	52	51.5	86	2 S54912	Ig heavy chain V r
39	49	48.5	229	2 S18605	hypothetical prote
40	47	46.5	98	2 PH0871	Ig heavy chain V r
41	47	46.5	131	2 S21924	Ig heavy chain V r
42	47	46.5	150	2 P40105	Ig heavy chain V r
43	47	46.5	789	2 F71161	anti-PR2 erythrocy
44	46.5	46.0	6486	2 T31076	probable chemotacti
45	46	45.5	79	2 A49021	tyrocidine synthet
					Ig heavy chain V-X

#### ALIGNMENTS

##### RESULT 1

D24672 Ig heavy chain V region (VGA03-8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999

C:Accession: D24672

R:Winter, E.; Radbruch, A.; Krawinkel, U.  
EMBO J. 4, 2861-2867, 1985

A:Reference number: A91022; MUID:86055722; PMID:2998759

A:Accession: D24672

A:Molecule type: DNA

A:Residues: 1-101 <WIN>  
A:Cross-references: GB:X03301; NID:G51757; PID:CAA27040.1; PID:G773215

A>Note: this sequence was determined from the differentiated gene

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999

C:Accession: S24764; S24772; S24777

R:Klages, S.  
submitted to the EMBL Data Library, August 1992

A:Reference number: S24763

A:Accession: S24764

A:Molecule type: DNA

A:Residues: 1-105 <KLA>  
A:Cross-references: EMBL:Z14999

A:Accession: S24772

A:Molecule type: DNA

A:Residues: 1-105 <KLM>  
A:Cross-references: EMBL:Z15011

R:Thomas, J.W.  
submitted to the EMBL Data Library, August 1992

A:Reference number: S24776

A:Accession: S24777

A:Molecule type: DNA

A:Residues: 1-105 <THO>  
A:Cross-references: EMBL:Z15020; NID:G52616; PID:CAA78739.1; PID:G52617

C:Genetics:  
A:introns: 9/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 93.1%; Score 94; DB 2; Length 105;  
Best Local Similarity 94.1%; Pred. No. 1.7e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17  
Db 62 WINTYGEPTVADDFKG 78

## RESULT 3

Ig heavy chain V region (subgroup XI) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999  
C/Accession: S24765; S24773; S24778  
R:Klages, S.

submitted to the EMBL Data Library, August 1992

A:Reference number: S24763

A:Accession: S24765

A:Molecule type: DNA

A:Residues: 1-105 <KLA>

A:Cross-references: EMBL:Z15001

A:Accession: S24773

A:Molecule type: DNA

A:Residues: 1-105 <KLM>

A:Cross-references: EMBL:Z15013

R:Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A:Reference number: S24776

A:Accession: S24778

A:Molecule type: DNA

A:Residues: 1-105 <THO>

A:Cross-references: EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PTD:G52620

C:Genetics:

A:Insertions: 9/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 93.1%; Score 94; DB 2; Length 105;  
Best Local Similarity 94.1%; Pred. No. 1.7e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17  
Db 62 WINTYGEPTVADDFKG 78

## RESULT 4

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C/Accession: S26325

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein

A:Reference number: S26309; PMID:91341421; PMID:1908510

A:Accession: S26325

A:Molecule type: mRNA

A:Status: preliminary

A:Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:G52080; PID:q1334043

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:5-88/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 94; DB 2; Length 109;  
Best Local Similarity 94.1%; Pred. No. 1.8e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17  
Db 40 WINTYGEPTVADDFKG 56

## RESULT 5

Ig heavy chain V region (M-T406) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004

C/Accession: S19967

R:Weissenborn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mb.

A:Reference number: S19963

A:Accession: S19967

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <WEI>

A:Cross-references: UNIPROT:Q921A6; EMBL:X65090

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:12-95/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 94; DB 2; Length 118;  
Best Local Similarity 94.1%; Pred. No. 1.9e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17  
Db 47 WINTYGEPTVADDFKG 63

## RESULT 6

Ig heavy chain V and J regions, monoclonal antibody SCER.M8.1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000

C/Accession: A53285

R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

Mol. Immunol. 28, 1063-1072, 1991

A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary struct

and their pH-reactivity profiles.

A:Reference number: A53285; PMID:92017897; PMID:1922102

A:Accession: A53285

A:Status: preliminary

A:Molecule type: DNA; protein

A:Residues: 1-119 <SAM>

A:Cross-references: GB:D12736; NID:G220595; PIDN:BA02228.1; PTD:G220596

A>Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBIIP:63299)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 94; DB 2; Length 119;  
Best Local Similarity 94.1%; Pred. No. 2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17  
Db 50 WINTYGEPTVADDFKG 66

## RESULT 7

Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jan-2000

C/Accession: PH1404; PH1406

R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Tai

J. Exp. Med. 176, 1209-1214, 1992

A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in t

A:Reference number: PH1403; MUID:93018837; PMID:1402663  
A:Accession: PH1404  
A:Molecule type: DNA  
A:Residues: 1-124 <SH1>  
A:Accession: PH1406  
A:Molecule type: DNA  
A:Residues: 115-121 <SH2>  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:35-118/Domain: immunoglobulin homology <IMM>

Query Match 93.1%; Score 94; DB 2; Length 124;  
Best Local Similarity 94.1%; Pred. No. 2e-07; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGPTVADDFKG 17  
|||  
Db 70 WINTYTGPTVADDFKG 86

RESULT 8  
S19968  
Ig heavy chain V region (M-T408) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S19968  
R:Weissenborn, W.; Rietmueler, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mb.  
A:Reference number: S19963  
A:Accession: S19968  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-115 <WE1>  
A:Cross-references: UNIPROT:Q921A6; EMBL:X65089  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 90.1%; Score 91; DB 2; Length 115;  
Best Local Similarity 88.2%; Pred. No. 5.5e-07; Indels 0; Gaps 0;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGPTVADDFKG 17  
|||  
Db 45 WINTYTGPTVADDFKG 61

RESULT 9  
B42848  
L6 mAb heavy chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: B42848; S33903  
R:Feil, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo  
J. Biol. Chem. 267, 15552-15558, 1992  
A:Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character  
A:Reference number: A42848; MUID:92348410; PMID:1639794  
A:Accession: B42848  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-120 <FE1>  
A:Cross-references: GB:M90690; NID:G195065; PIDN:AAA38146.1; PID:G195066  
A>Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBI:P:109961)  
A:Accession: S33903  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <FE2>  
A:Cross-references: EMBL:M90691  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.1%; Score 91; DB 2; Length 120;  
Best Local Similarity 88.2%; Pred. No. 5.8e-07; Indels 0; Gaps 0;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGPTVADDFKG 17  
|||  
Db 50 WINTYTGPTVADDFKG 66

RESULT 10  
S33905  
Ig heavy chain precursor V region - synthetic  
C:Species: synthetic  
C>Date: 13-Jan-1995 #sequence\_revision 30-Apr-1998 #text\_change 20-Oct-2000  
C:Accession: S33905  
R:Lin, A.Y.; Robinson, R.R.; Hellstroem, K.E.; Murray Jr., E.D.; Chang, C.P.; Hellstroem  
Proc. Natl. Acad. Sci. U.S.A. 84, 3439-3443, 1987  
A:Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.  
A:Reference number: S33905; MUID:87204152; PMID:3106970  
A:Accession: S33905  
A:Molecule type: mRNA  
A:Residues: 1-146 <LIU>  
A:Cross-references: EMBL:M6072; NID:G195270; PIDN:AAA38229.1; PID:G195271

Query Match 90.1%; Score 91; DB 4; Length 146;  
Best Local Similarity 88.2%; Pred. No. 7.1e-07; Indels 0; Gaps 0;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYTGPTVADDFKG 17  
|||  
Db 69 WINTYTGPTVADDFKG 85

RESULT 11  
C32530  
Ig heavy chain V region (10/8) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 16-Aug-1996  
C:Accession: C32530  
R:Deverson, E.; Berlek, C.; Taussig, M.; Feinstein, A.  
Eur. J. Immunol. 17, 9-13, 1987  
A:Title: Monoclonal BALB/c anti-progesterone antibodies use family IX variable region he  
A:Reference number: A32530; MUID:87133855; PMID:3102254  
A:Accession: C32530  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <DEV>  
A:Cross-references: GB:M27585  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 89.1%; Score 90; DB 2; Length 102;  
Best Local Similarity 88.2%; Pred. No. 7e-07; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WINTYTGPTVADDFKG 17  
|||  
Db 33 WINTYTGPTVADDFKG 49

RESULT 12  
S24766  
Ig heavy chain V region (subgroup XI) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 21-Nov-1998 #text\_change 23-Jul-1999  
C:Accession: S24766; S24774; S24779  
R:Klages, S.  
submitted to the EMBL Data Library, August 1992  
A:Reference number: S24766  
A:Accession: S24766  
A:Molecule type: DNA  
A:Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z15002  
A/Accession: S24774  
A/Molecule type: DNA  
A/Residues: 1-105 <KLM>  
A/Cross-references: EMBL:Z15014  
R/Thomas, J.W.  
Submitted to the EMBL Data Library, August 1992  
A/Reference number: S24776  
A/Accession: S24779  
A/Molecule type: DNA  
A/Residues: 1-105 <THO>  
A/Cross-references: EMBL:Z15023; NID:952621; PIDN:CAA78742.1; PID:952622  
C/Genetics:  
A/Intitons: 9/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 84.2%; Score 85; DB 2; Length 105;  
Best Local Similarity 88.2%; Pred. No. 4.3e-06;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
DB 62 WINTYGEPTYADDFKG 78

RESULT 13  
A32530  
Ig heavy chain V region (DB3) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 21-Jan-2000  
C/Accession: A32530  
R/Deverson, E.; Berék, C.; Tauszig, M.; Feinstein, A.  
Eur. J. Immunol. 17, 9-13, 1987  
A/Title: Monoclonal BAIB/C anti-progesterone antibodies use family IX variable region he  
A/Reference number: A32530; MUID:67133855; PMID:3102254  
A/Accession: A32530  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-118 <DEV>  
A/Cross-references: GB:M27583  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 84; DB 2; Length 118;  
Best Local Similarity 82.4%; Pred. No. 6.9e-06;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
DB 49 WINTYGEPTYADDFKG 65

RESULT 14  
D32967  
Ig heavy chain V region TE32 - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 21-Jan-2000  
C/Accession: D32967  
R/Levy, R.; Asulin, O.; Scherf, T.; Levitz, M.; Anglister, J.  
Biochemistry 28, 7168-7175, 1989  
A/Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predi  
A/Reference number: A32967; MUID:90057406; PMID:2819059  
A/Accession: D32967  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: mRNA  
A/Residues: 1-114 <LEV>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.2%; Score 83; DB 2; Length 114;

Best Local Similarity 82.4%; Pred. No. 9.6e-06;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
DB 50 WINTYSGVPTVADDFKG 66

RESULT 15  
C32967  
Ig heavy chain V region TE33 - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 21-Jan-2000  
C/Accession: C32967  
R/Levy, R.; Asulin, O.; Scherf, T.; Levitz, M.; Anglister, J.  
Biochemistry 28, 7168-7175, 1989  
A/Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predi  
A/Reference number: A32967; MUID:90057406; PMID:2819059  
A/Accession: C32967  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: mRNA  
A/Residues: 1-114 <LEV>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.2%; Score 83; DB 2; Length 114;  
Best Local Similarity 82.4%; Pred. No. 9.6e-06;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WINTYGEPTYAGDFKG 17  
DB 50 WINTYSGVPTVADDFKG 66

Search completed: March 1, 2005, 17:44:44  
Job time : 24.0154 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 110.108 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-16  
Perfect score: 101  
Sequence: 1 WINTYGEPTVAGDPFGK 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	94	93.1	241 2	Q921A6
2	85	84.2	102 2	Q9JL79
3	80	79.2	116 2	Q683Y7
4	80	79.2	116 2	Q683Y8
5	79	78.2	140 2	Q652L3
6	71	70.3	125 2	Q6PIL0
7	67	66.3	218 2	Q925S1
8	65	64.4	484 2	Q991A6
9	56	55.4	1549 2	Q76D19
10	49	48.5	229 2	Q9XU00
11	48	48.5	763 1	THED CORGL
12	48	47.5	600 2	Q9B096
13	47	46.5	192 2	Q8PCD7
14	47	46.5	322 2	Q857U4
15	47	46.5	732 2	Q6LND6
16	47	46.5	739 2	Q8B7Y9
17	47	46.5	2151 2	Q6L725
18	47	46.5	3399 2	Q6L725
19	46.5	46.0	6486 1	TYCC BREPA
20	46	45.5	150 1	GRDA_CLOPU
21	46	45.5	379 2	Q87G18
22	46	45.5	500 2	Q6N091
23	46	45.5	598 2	Q857J4
24	46	45.5	617 2	Q8Y6K6
25	46	45.5	617 2	Q92AY2
26	46	45.5	617 2	Q711Y9
27	46	45.5	618 2	Q9KCE2
28	46	45.5	739 1	THED CORFP
29	46	45.5	739 1	Q8JVD0
30	45	44.6	389 2	Q752V2
31	45	44.6	411 2	Q6PPG2

32	45	44.6	419 2	Q6IO97	Q61q97 brachydanio
33	45	44.6	419 2	Q7ZV02	Q7ZV02 brachydanio
34	45	44.6	469 2	Q7Z7P5	Q7Z7P5 homo sapien
35	45	44.6	487 2	Q6QBS6	Q6QBS6 chlamydomon
36	45	44.6	518 2	Q6N030	Q6N030 homo sapien
37	45	44.6	585 2	Q6UE12	Q6UE12 lactobacill
38	45	44.6	591 2	Q74JU8	Q74JU8 lactobacill
39	45	44.6	614 2	Q8DX11	Q8DX11 streptococc
40	45	44.6	614 2	Q8E2W0	Q8E2W0 streptococc
41	45	44.6	839 2	Q19198	Q19198 caenorhabdi
42	45	44.6	842 2	Q65ZH7	Q65ZH7 caenorhabdi
43	45	44.6	868 2	Q8A2M9	Q8A2M9 bacteroides
44	45	44.6	2009 2	Q7N848	Q7N848 photobacter
45	44.5	44.1	309 2	Q8R7D4	Q8R7D4 thermosaneer

## ALIGNMENTS

RESULT 1				
ID	Q921A6	PRELIMINARY;	PRT;	241 AA.
AC	Q921A6;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Anti-CBA 79 single chain Fv (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=98170165; PubMed=9509426;			
RX	Chung J.H., Choi S.J., Kim H.J., Kim I.J., Lee S.D.,			
RY	Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;			
RT	"Cloning and characterization of cDNAs encoding VH and VL of a			
RT	monoclonal anti-CBA antibody (CBA 79) cross-reactive with NCA-95 and			
RT	generation of a single-chain Fv molecule (scFv)."			
RL	Mol. Cells 7:816-819 (1997).			
DR	EMBL; U88067; AAB4804.1; -.			
DR	PIR; S19965; S19965.			
DR	PIR; S19967; S19967.			
DR	PIR; S19968; S19968.			
DR	PIR; S26325; S26325.			
DR	HSSP; P01607; 1BMW.			
DR	SMART; SM00406; IGV; 2.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
FT	NON_TER	1	1	
FT	NON_TER	241	241	
FT	SEQUENCE	241 AA;	26086 MW;	Q276887248B9C771 CRC64;
Query Match				
Best Local Similarity 93.1%; Score 94; DB 2; Length 241;				
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
RESULT 2				
ID	Q9JL79	PRELIMINARY;	PRT;	102 AA.
AC	Q9JL79;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Anti-myosin immunoglobulin heavy chain variable region			
DE	(Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A.CA.  
 RX MEDLINE=20448942; PubMed=10992488;  
 RA DOI=10.1128/IAI.68.10.5803-5808.2000;  
 RA Makiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "T-Cell-dependent antibody response to the dominant epitope of  
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
 RT with cardiac myosin."  
 RL Infect. Immun. 68:5803-5808(2000).  
 DR EMBL; AF206027; AAF69325.1; -.  
 DR HSSP; P01751; INOB.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT 102 102  
 SQ SEQUENCE 102 AA; 11543 MW; ES90C292093F6711 CRC64;

Query Match 84.2%; Score 85; DB 2; Length 102;  
 Best Local Similarity 88.2%; Pred. No. 6.8e-06;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WINTYGEPTVAGDFKG 17  
 |||||  
 DB 35 WINTGTGEPYADDFKG 51

RESULT 3  
 O683Y7 PRELIMINARY; PRT; 116 AA.

AC O683Y7;  
 DT 25-OCT-2004 (TEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)  
 DE Immunoglobulin heavy chain variable region (Fragment).

GN Name=IGHV;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Balb/c;  
 RA Phalipon A., Costachel C., Thuitat A., Nato F.;  
 RT "Anti-11popolysaccharide antibodies protective against Shigella  
 RT flexneri 2a infection recognize an immunodominant serotype-specific  
 RT determinant on the O-antigen."  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ784033; CAH04483.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00409; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1  
 FT 116 116  
 SQ SEQUENCE 116 AA; 12863 MW; SECL1AD02E911952 CRC64;

Query Match 79.2%; Score 80; DB 2; Length 116;  
 Best Local Similarity 82.4%; Pred. No. 5.1e-05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WINTYGEPTVAGDFKG 17  
 |||||  
 DB 50 WINTGTGEPYADDFKG 66

RESULT 4

O683Y8 PRELIMINARY; PRT; 116 AA.

AC O683Y8;  
 DT 25-OCT-2004 (TEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)  
 DE Immunoglobulin heavy chain variable region (Fragment).

GN Name=IGHV;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Balb/c;  
 RA Phalipon A., Costachel C., Thuitat A., Nato F.;  
 RT "Anti-11popolysaccharide antibodies protective against Shigella  
 RT flexneri 2a infection recognize an immunodominant serotype-specific  
 RT determinant on the O-antigen."  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ784032; CAH04482.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00409; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1  
 FT 116 116  
 SQ SEQUENCE 116 AA; 12833 MW; C85932C0D843778D CRC64;

Query Match 79.2%; Score 80; DB 2; Length 116;  
 Best Local Similarity 82.4%; Pred. No. 5.1e-05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WINTYGEPTVAGDFKG 17  
 |||||  
 DB 50 WINTATGEPYADDFKG 66

RESULT 5

O65ZL3 PRELIMINARY; PRT; 140 AA.

AC O65ZL3;  
 DT 25-OCT-2004 (TEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)  
 DE Tg10H (Fragment).

GN Name=Tg10H;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC MEDLINE=96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;  
 RA Noel D., Bernardi T., Navarro-Teulon I., Marin M., Martinetto J.P.,  
 RA Ducancel F., Mani J.C., Pau B., Plechaczkyk M., Biad-Plechaczkyk M.;  
 RT "Analysis of the individual contributions of immunoglobulin heavy and  
 RT light chains to the binding of antigen using cell transfection and  
 RT plasmon resonance analysis."  
 RL J. Immunol. Methods 193:177-187(1996).

DR EMBL; S82492; AAB37434.2; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00409; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 140  
 FT 140 140  
 SQ SEQUENCE 140 AA; 15302 MW; 7BFE237F3D965F43 CRC64;

Query Match 78.2%; Score 79; DB 2; Length 140;



Best Local Similarity 76.5%; Pred. No. 9e-05;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WINTYGEPTVAGDPFG 17  
Db 69 WINTPSGVPTVADDFPG 85

## RESULT 6

06PIL0 PRELIMINARY; PRT; 125 AA.  
AC 06PIL0  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
NCBI\_TaxId=9606;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Maira M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC032733; AAH32733.1; -  
DR HSSP: P01751; 1A6W.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003596; IG\_v.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG-LIKE; 1.  
KM Hypothetical protein\_125 AA; 13913 MW; B76CE34F5A69788 CRC64;  
SQ SEQUENCE 125 AA; 13913 MW; B76CE34F5A69788 CRC64;

Query Match 70.3%; Score 71; DB 2; Length 125;  
Best Local Similarity 70.6%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WINTYGEPTVAGDPFG 17  
Db 69 WINTYGNPTVYAGQFTG 85

## RESULT 7

0925S1 PRELIMINARY; PRT; 218 AA.  
AC 0925S1  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE MRPS (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
RA Su C.,  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
RT the repair of intestinal epithelium after irradiation in mice."  
RL World J. Gastroenterol. 6:709-717(2000).  
[2]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.,  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of mice of  
RT the same strain."  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL: AF240168; AAK43733.1; -  
DR HSSP: P01655; 10NZ.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG-LIKE; 1.  
FT NON-TER 218  
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 66.3%; Score 67; DB 2; Length 218;  
Best Local Similarity 66.7%; Pred. No. 0.013;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WINTYGEPTVAGDPFG 17  
Db 52 WINTHSGVPTVYAEFG 68

## RESULT 8

099LA6 PRELIMINARY; PRT; 484 AA.  
AC 099LA6  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=mlx FVB/N; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Maira M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human

RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	12]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=mix EVE/N; TISSUE=Mammary tumor;		
RA	Strasbourg R.;		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC003495; AAH03495.1; -		
DR	PIR; F33932; F33932.		
DR	PIR; S19963; S19963.		
DR	HSSP: P01810; 2FBT.		
DR	InterPro; IPR007110; Ig_1like.		
DR	InterPro; IPR003597; Ig_C1.		
DR	InterPro; IPR003506; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF07654; C1-set; 2.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PSS0835; IG_LIKE; 4.		
DR	PROSITE; PSS00290; IG_MHC; UNKNOWN_2.		
KW	Hypothetical protein.		
QO	SEQUENCE 484 AA; 52667 MW; 8EA4E4F9BCF582DA CRC64;		

Query Match	64.4%	Score 65	DB 2	Length 484
Best Local Similarity	64.7%	Pred. No. 0.064		
Matches	11	Conservative	1	Mismatches 5
				Indels 0
				Gaps 0
Qy	1	WINTYTGEPYACDPFG	17	
	:			
	:			
	:			
Db	69	WVNIEGTGSYVADDFKG	85	

RESULT 9	
Q76D19	
ID Q76D19	PRELIMINARY;
	PRT; 1549 AA

DT	05-JUL-2004 (TREMBLrel. 27, Created)	
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
DE	Beta-N-acetylglucosaminidase (EC 3.2.1.52).	
GN	Name=nag94A;	
OS	Clostridium paraputrificium.	
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.	
OC	Clostridium.	
OX	NCBI_TaxId=29363;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Li H., Morimoto K., Kimura T., Sakka K., Lun S., Ohmura K.;	
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.	
CC	1-SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by	
CC	an amide bond (By similarity).	
EMBL	AB100099, BAC98989, 1--.	
GO	GO:0009866; C:cell surface; IEA.	
GO	GO:0004563; F:beta-N-acetylhexosaminidase activity; IEA.	
GO	GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.	
GO	GO:0005875; P:carbohydrate metabolism; IEA.	
GO	GO:0007155; P:cell adhesion; IEA.	
DR	InterPro: IPR000421, Pfam C.	
DR	InterPro: IPR011480, Pfam F.	
DR	InterPro: IPR011899, Gram_pos_anchor.	
DR	InterPro: IPR011496, Hyalase.	
DR	Pfam: PF00754, F5_F8_type_C, 2.	
DR	Pfam: PF07554, FIVAR, 2.	
DR	Pfam: PF00746; Gram_pos_anchor, 1.	
DR	Pfam: PF07555; Hyaluronidase, 2; 1.	
DR	TIGRfam: TIGR01167, LPTXG_anchor, 1.	
DR	PROSITE: PS50022, FAS8C_3, 1.	
KW	Cell wall; Glycosidase; Hydrolyase; Peptidoglycan-anchor.	
QO	SEQUENCE, 1549 AA; 173412 MW; C6AF8B2D96D47285 CRC64;	

Query Match	55.4%	Score 56	DB 2	length 1549
Best Local Similarity	58.8%	Pred. No.	6.5	
Matches 10	Conservative 1	Mismatches 6	Indels 0	Gaps 0

QY 1 WINTYTGEPTYAGDFKG 17  
| | : | | | | | |  
Db 840 WYKTNDDGDMTYAGDFVG 856

RESULT 10  
Q9XUA0  
ID Q9XUA0  
PRELIMINARY;  
PRT; 229 AA

DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein AC8.7.  
GN ORFNames=AC8.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae.  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RP STRAIN=Bristol N2.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "genome sequence of the nematode C.elegans: A platform for  
RT investigating biology."  
RL Science 282:2012-2018 (1998).  
[2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RP STRAIN=Bristol N2;  
RA McMurray A.A.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z883097; CAB05453.1; -.  
DR PIR; T18605; T18605.  
DR WormBase; WBGene00007079; AC8.7.  
DR WormPep; AC8.7; CB20441.  
DR Hypothetical protein.  
SQ SEQUENCE 229 AA; 26193 MW; 5520C31D3F1930C8 CRC64;

Query Match	48.5%	Score	49	DB	2	Length	229
Best Local Similarity	41.2%	Pred. No.	12				
Matches	7	Conservative	3	Mismatches	7	Indels	0
						Gaps	0

```
QY      1 WINTYTGEPTYAGDEKG 17
        | : | : | : |
Db      31 WVRKIPGQKPYLGDKG 47
```

RESULT 11	
THED_CORGL	
ID THED_CORGL	STANDARD; PRT; 763 AA

DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, last sequence update)  
DT 25-OCT-2004 (Rel. 45, last annotation update)  
DE Multifunctional protein chid1 (includes: Thiamine-phosphate  
DE pyrophosphorylase [EC 2.5.1.3] (TMP pyrophosphorylase) (TMP-Pase)  
DE (thiamine-phosphate synthetase) ; Phosphomethylpyrimidine kinase  
DE [EC 2.7.4.7] (HMP-phosphate kinase) (HMP-P kinase)].  
GN Name(s): Synonyms=chid1; OrderedAccession=CG11463, cg1654;  
OS Corynebacterium glutamicum (Brevibacterium flavum)  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxId=1718;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
RC "Nagagawa S. ;  
RA "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032." ;  
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
XC PubMed=12948626; DOI=10.1016/S0166-1656(03)00154-8;

RA Kalinowski J., Bathe B., Bartels D., Biechoff N., Bott M.,  
 RA Bukowski A., Dusch N., Eggeling L., Elkmann B.J., Gaijalat L.,  
 RA Goessmann A., Hartmann M., Hutmacher K., Kraemer R., Linke B.,  
 RA McIlrath A.C., Meyer F., Moeckel B., Pfeifferle W., Puchler A.,  
 RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,  
 RA Tauch A.,  
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence  
 RT and its impact on the production of L-aspartate-derived amino acids  
 RT and vitamins.",  
 RL J. Biotechnol. 104:5-25 (2003).  
 CC -1- FUNCTION: Condenses 4-methyl-5-(beta-hydroxyethyl)-thiazole  
 CC monophosphate (TH2-P) and 4-amino-5-hydroxymethyl pyrimidine  
 CC pyrophosphate (HMP-PP) to form thiamine monophosphate (TMP) (By  
 CC similarity).  
 CC -1- FUNCTION: Catalyzes the phosphorylation of HMP-P to HMP-PP (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: 2-methyl-4-amino-5-hydroxymethylpyrimidine  
 CC di-phosphate + 4-methyl-5-(2-phosphono-oxyethyl)-thiazole =  
 CC -1- CATALYTIC ACTIVITY: ATP + 4-amino-2-methyl-5-  
 CC phosphomethylpyrimidine = ADP + 4-amino-2-methyl-5-  
 CC di-phosphomethylpyrimidine.  
 CC -1- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).  
 CC -1- PATHWAY: Thiamine biosynthesis.  
 CC -1- SIMILARITY: In the N-terminal section; belongs to the TMP-PPase  
 CC family.  
 CC -1- SIMILARITY: In the middle section; belongs to the thid family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: AP005278; BAB98856.1; ALT\_INIT.  
 DR EMBL: BX927152; CAP21472.1; -.  
 DR HSSP: P55882; LUXH.  
 DR HAMAP: MF\_00097; fused. 1.  
 DR InterPro: IPR004393; HMP-P\_kinase.  
 DR InterPro: IPR002173; PFkB-  
 DR InterPro: IPR004305; TENA\_THI-4.  
 DR Pfam: PF00294; PFkB. 1.  
 DR Pfam: PF03070; TENA\_THI-4. 1.  
 DR ProDom: PD19806; TMP\_synthase. 1.  
 DR TRIGRAMS: TRIGR00097; HMP-P\_kinase. 1.  
 KW Complete proteome; Magnesium; Metal-binding; Multifunctional enzyme;  
 KM Thiamine biosynthesis; Transferrase.  
 FT DOMAIN 1 210 Thiamine-phosphate pyrophosphorylase.  
 FT DOMAIN 245 500 Phosphomethylpyrimidine kinase.  
 FT METAL 550 763 Unknown.  
 FT METAL 70 70 Magnesium (By similarity).  
 FT METAL 88 88 Magnesium (By similarity).  
 SQ SEQUENCE 763 AA; 80355 MW; CA992321E84577F CRC64;

Query Match 48.5%; Score 49; DB 1; Length 763;  
 Best Local Similarity 61.5%; Pred. No. 42;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 WINTYGEPTYAG 13  
 Db 699 WINTYGEPTIAG 711

RESULT 12  
 ID Q9B096 PRELIMINARY; PRT; 600 AA.  
 AC Q9B096;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Gp25.

OS Mycobacteriophage Bxb1.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
 NC NCBI\_TaxID=148603;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20572070; PubMed=11123671;  
 RA Mediavilla J., Jain S., Kriakov J., Ford M.E., Duda R.L., Jacobs W.R.,  
 RA Hendrix R.W., Hatfull G.F.;  
 RT "Genome organization and characterization of mycobacteriophage Bxb1."  
 RL Mol. Microbiol. 38:955-970 (2000).  
 DR EMBL: AF271693; AAG59730.1; -.  
 SQ SEQUENCE 600 AA; 66895 MW; F98F693F1BAECB9 CRC64;

Query Match 47.5%; Score 48; DB 2; Length 600;  
 Best Local Similarity 57.1%; Pred. No. 48;  
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 2 INTYGEPTYAGDF 15  
 Db 325 IDITYGLPTPGEX 338

RESULT 13  
 ID Q8PCD7 PRELIMINARY; PRT; 192 AA.  
 AC Q8PCD7;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Hypothetical protein XCC0797.  
 GN Ordered locus names: XCC0797;  
 OS Xanthomonas campestris (pv. campestris).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 NC NCBI\_TaxID=340;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPRATN-ATCC 33913 / NCPPB 528;  
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
 RA da Silva A.C.R., Ferris J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
 RA Camarotte G., Camavari F., Cardozo J., Chambergo F., Clapina L.P.,  
 RA Cicarelli R.M.B., Coutinho L.B., Cursino-Santos J.R., El-Dorri H.,  
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Pietro M.I.T.,  
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kiehl L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities."  
 RL Nature 417:459-463 (2002).  
 DR EMBL: AB012179; AAM40112.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 192 AA; 21202 MW; DDF149BC7EB01772 CRC64;

Query Match 46.5%; Score 47; DB 2; Length 192;  
 Best Local Similarity 56.2%; Pred. No. 21;  
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WINTYGEPTYAGDF 16  
 Db 137 WISASVAPETIAGMK 152

RESULT 14  
 ID Q857U4 PRELIMINARY; PRT; 322 AA.  
 Q857U4

AC Q857U4; 01-JUN-2003 (TrEMBLrel: 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel: 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel: 24, Last annotation update)  
 DE Gp68.  
 OS Mycobacteriophage Cw1.  
 OC Viruses; dsDNA viruses; no RNA stage; Caudovirales; Siphoviridae.  
 OX NCBI\_TaxID=205869;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;  
 RA Pedulla M.L., Ford M.B., Houtz J.M., Karkhakeyan T., Wadsworth C.,  
 RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,  
 RA Brucker W., Kumar V., Kandamany J., Keenan L., Bardarov S.,  
 RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,  
 RA Hatfull G.F.;  
 RT "Origins of highly mosaic mycobacteriophage genomes."  
 RL Cell 113:171-182(2003).  
 DR EMBL; AY129331; AAN01682.1; -.  
 SQ SEQUENCE 322 AA; 36011 MW; 96F4AA48392A2112 CRC64;

Query Match 46.5%; Score 47; DB 2; Length 322;  
 Best Local Similarity 56.2%; Pred. No. 36;  
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 INTYGEPTYAGDFKG 17  
 DB 93 INEYDGDPPYKGGDGG 108

## RESULT 15

06LN06 PRELIMINARY; PRT; 732 AA.  
 ID 06LN06  
 AC 06LN06  
 DT 05-JUL-2004 (TrEMBLrel: 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel: 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel: 27, Last annotation update)  
 DE Hypothetical protein VP0215.  
 GN Name=VP0215; OrderedLocuNames=BPAPA2692;  
 OS Photobacterium profundum (Photobacterium sp. (strain SS9)).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Photobacterium.  
 OX NCBI\_TaxID=74109;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,  
 RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,  
 RA Valle G.;  
 RT "Genome analysis of Photobacterium profundum reveals the complexity of  
 RT high pressure adaptations."  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR378671; CAG21070.1; -.  
 DR InterPro: IPR010344; DUF940.  
 DR Pfam: PF06082; DUF940; 1.  
 DR Complete proteome; Hypothetical protein.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 732 AA; 82241 MW; 2B59D154977B3DDF CRC64;

Query Match 46.5%; Score 47; DB 2; Length 732;  
 Best Local Similarity 58.3%; Pred. No. 86;  
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 YTGEPYAGDFK 16  
 DB 95 YGDPYFSGDTK 106

Search completed: March 1, 2005, 17:43:13  
 Job time : 113.108 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 89.7231 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-17

Perfect score: 76

Sequence: 1 EGFGCHRGPDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	12	3	AAV32225
2	52	68.4	121	8	ADP22288
3	52	68.4	121	8	ADP22296
4	51	67.1	121	8	ADP22284
5	46	60.5	331	7	ADP60921
6	46	60.5	331	8	ADP19157
7	46	60.5	331	8	ADP54207
8	46	60.5	331	8	ADP23166
9	46	60.5	332	5	ABP69582
10	46	60.5	332	7	ADG77005
11	46	60.5	332	7	ADG77005
12	46	60.5	332	8	AD126203
13	46	60.5	336	4	ABG18625
14	46	60.5	701	7	ABO81895
15	45	59.2	121	8	ADP22190
16	45	59.2	121	8	ADP22186
17	45	59.2	158	8	ADK47356
18	45	59.2	170	8	ADR95130
19	45	59.2	387	4	ABG26863
20	45	59.2	427	4	ABG29887
21	45	59.2	495	4	ABB65066
22	45	59.2	569	7	ABO83544
23	45	59.2	944	6	ABB80172
24	44	57.9	47	6	ADA23219
25	44	57.9	77	6	ADA23218

26	44	57.9	458	6	ABU22342	ABU22342	Protein e
27	43	56.6	90	5	ABP04474	ABP04474	Human ORF
28	43	56.6	1583	8	ADU48668	ADU48668	Oil-aseoc
29	43	56.6	1724	8	ADU50155	ADU50155	Oil-aseoc
30	43	56.6	1897	4	AAU15088	AAU15088	Protein e
31	43	56.6	1897	5	ABP73203	ABP73203	Candida a
32	42	55.3	905	8	ABM82633	ABM82633	Human dia
33	42	55.3	934	5	ABR06112	ABR06112	Human NS
34	42	55.3	934	8	ABM82632	ABM82632	Human dia
35	42	55.3	935	8	ABM82631	ABM82631	Human dia
36	42	55.3	979	2	AAV06606	AAV06606	Human isl
37	42	55.3	979	4	AAAG80205	AAAG80205	Human aut
38	42	55.3	979	6	ABU04793	ABU04793	Human exp
39	42	55.3	979	6	ABU04784	ABU04784	Human exp
40	42	55.3	979	6	ABU04789	ABU04789	Human exp
41	42	55.3	979	6	ABU04794	ABU04794	Human exp
42	42	55.3	979	7	ADP57230	ADP57230	Human pro
43	42	55.3	979	7	ADP56167	ADP56167	Human pro
44	42	55.3	979	7	ADP57226	ADP57226	Human pro
45	42	55.3	979	7	ADD45278	ADD45278	Human pro

## ALIGNMENTS

RESULT 1	AAV32225	standard; peptide; 12 AA.
XX	AAV32225;	
XX	15-FEB-2000	(first entry)
XX	G-CSF agonist antibody mAb163-93 heavy chain variable region CDR3.	
XX	Granulocyte colony stimulating factor receptor; G-CSF, mouse;	
XX	monoclonal antibody; agonist; screening; neutropenia; therapy;	
XX	complementarity determining region; CDR; mAb163-93.	
XX	Mus musculus.	
XX	MO9955735-A1.	
XX	04-NOV-1999.	
XX	30-APR-1999;	99WO-US009466.
XX	30-APR-1998;	98US-0083575P.
XX	(TANO-) TANOX INC.	
XX	Ni B, Sun BNC, Sun CRY;	
XX	WPI; 2000-052805/04.	
XX	Treatment of neutropenia by stimulating proliferation of neutrophilic	
XX	cell lineage progenitors.	
XX	Claim 13; Page 30; 64pp; English.	
XX	The present sequence represents complementarity determining region 3	
XX	(CDR3) of the heavy chain variable region of murine monoclonal antibody	
XX	mAb163-93. This antibody is an example of an agonist molecule that	
XX	specifically binds to or interacts with human granulocyte colony	
XX	stimulating factor (G-CSF) receptor to stimulate cell proliferation and	
XX	differentiation, especially by dimerising the receptor or activating	
XX	phosphorylation of kinases associated with the receptor. Agonist	
XX	antibodies can be used to stimulate proliferation of G-CSF-dependent	
XX	cells, e.g. to differentiate leading to a repopulation of neutrophilic	
XX	granulocyte lineage cells, especially to treat neutropenia (claimed).	
XX	They can also be used to detect human G-CSF receptor immunologically	
XX	Sequence 12 AA;	
XX		

Query Match 100.0%; Score 76; DB 3; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGFYGGHPGPDY 12  
 |||||  
 DB 1 EGFYGGHPGPDY 12

RESULT 2  
 ADP22288  
 ID ADP22288 standard; protein; 121 AA.  
 XX  
 AC ADP22288;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:194.

XX human: monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KM anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KM antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KM eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;  
 KM neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KM TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KM bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KM prostate cancer; immuno-mediated inflammatory disease;  
 KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KM restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KM septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.  
 OS  
 XX  
 PN WO2004050683-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038281.  
 XX  
 PR 02-DEC-2002; 2002US-0430729P.  
 XX

PA (ABGE-) ABGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX  
 DR MPI; 2004-480601/45.  
 DR N-PSDB; ADP22287.

XX  
 PT New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX

PS Example 10; SEQ ID NO 194; 213pp; English.

XX The present invention describes a human monoclonal antibody (1) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFA in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFA induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for

CC TNFA induced apoptosis by administering the human monoclonal antibody of  
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotoxic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (1) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 121 AA;

Query Match 68.4%; Score 52; DB 8; Length 121;  
 Best Local Similarity 75.0%; Pred. No. 2.8;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGFYGGHPGPDY 12  
 |||||  
 DB 99 EGDYGGYPYFDY 110

RESULT 3  
 ADP22296  
 ID ADP22296 standard; protein; 121 AA.  
 XX  
 AC ADP22296;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:202.

XX human: monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KM anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KM antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KM eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;  
 KM neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KM TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KM bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KM prostate cancer; immuno-mediated inflammatory disease;  
 KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KM restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KM septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.  
 OS  
 XX  
 PN WO2004050683-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038281.  
 XX  
 PR 02-DEC-2002; 2002US-0430729P.  
 XX

PA (ABGE-) ABGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX  
 DR MPI; 2004-480601/45.  
 DR N-PSDB; ADP22295.

XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid

PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 202; 213pp; English.  
 XX  
 CC The present invention describes a human monoclonal antibody (1) that  
 CC specifically binds to tumour necrosis factor- $\alpha$  (TNF $\alpha$ ) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNF $\alpha$  in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNF $\alpha$  in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNF $\alpha$  induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNF $\alpha$  induced apoptosis by administering the human monoclonal antibody of  
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNF $\alpha$  antagonist. The antibody (1) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC stomach cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNF $\alpha$   
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 121 AA;  
 Query March 68.4%; Score 52; DB 8; Length 121;  
 Best Local Similarity 75.0%; Pred. NO. 2.8;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EGFYGHGPFY 12  
 Db 99 EGDYGYRPFY 110  
 RESULT 4  
 ADP22284  
 ID ADP22284 standard; protein, 121 AA.  
 XX  
 AC ADP22284;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human anti-TNF $\alpha$  antibody heavy chain variable region SEQ ID NO:190.  
 XX  
 KW human, monoclonal antibody; tumour necrosis factor- $\alpha$ ; TNF $\alpha$ ;  
 KW anti-TNF $\alpha$  antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotropic; antiapoptotic; TNF $\alpha$  antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2004050683-A2.  
 XX

PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038281.  
 XX  
 PR 02-DEC-2002; 2002US-0430729P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Babcock JS, Kang JS, Foord O, Green L, Peng X, Klakamp S;  
 P1 Haak-Frendencho M, Rathnaswami P, Pigott C, Liang ML, Lee R,  
 P1 Marchalenchko K, Fagglioni R, Senaldi G, Qiaojuan JS;  
 XX  
 DR WPI: 2004-480601/45.  
 DR N-PSDB; ADP22283.  
 XX  
 XX New recombinant human monoclonal antibody that specifically binds to  
 FT Tumor Necrosis Factor- $\alpha$ , useful for treating neoplastic disease such  
 PT as cancer, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 190; 213pp; English.  
 XX  
 CC The present invention describes a human monoclonal antibody (1) that  
 CC specifically binds to tumour necrosis factor- $\alpha$  (TNF $\alpha$ ) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNF $\alpha$  in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNF $\alpha$  in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNF $\alpha$  induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNF $\alpha$  induced apoptosis by administering the human monoclonal antibody of  
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNF $\alpha$  antagonist. The antibody (1) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC stomach cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNF $\alpha$   
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 121 AA;  
 Query March 67.1%; Score 51; DB 8; Length 121;  
 Best Local Similarity 75.0%; Pred. NO. 4;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EGFYGHGPFY 12  
 Db 99 EGDYGYRPFY 110  
 RESULT 5  
 ADE60921  
 ID ADE60921 standard; protein, 331 AA.  
 XX  
 AC ADE60921;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Rat Protein NP\_112620, SEQ ID NO 6835.  
 XX

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX  
 XX Rattus norvegicus.  
 XX  
 XX WO2003016475-A2.  
 XX  
 XX 27-FEB-2003.  
 XX  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX  
 XX 14-AUG-2001; 2001US-0312147P.  
 XX 01-NOV-2001; 2001US-0346382P.  
 XX 26-NOV-2001; 2001US-033347P.  
 XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 XX (FARB ) BAYER AG.  
 XX  
 XX Woolf C, D'ureo D, Befort K, Costigan M;  
 XX  
 XX MPI; 2003-268312/26.  
 XX GENBANK; NF\_112620.  
 XX  
 XX New composition comprising two or more isolated polypeptides, useful for  
 XX preparing a medicament for treating pain in an animal.  
 XX  
 XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 XX or human polynucleotides or a polynucleotide which represents a fragment,  
 XX derivative or allelic variation of the nucleic acid sequence. Also  
 XX claimed are a vector comprising the novel polynucleotide, a host cell  
 XX comprising the vector, a method for identifying a nucleotide sequence  
 XX which is differentially regulated in an animal subjected to pain and a  
 XX kit to perform the method, an array, a method for identifying an agent  
 XX that increases or decreases the expression of the polynucleotide sequence  
 XX that is differentially expressed in neuronal tissue of a first animal  
 XX subjected to pain, a method for identifying a compound which regulates  
 XX the expression of a polynucleotide sequence which is differentially  
 XX expressed in an animal subjected to pain, a method for identifying a  
 XX compound that regulates the activity of one or more of the  
 XX polynucleotides, a method for producing a pharmaceutical composition, a  
 XX method for identifying a compound or small molecule that regulates the  
 XX activity in an animal of one or more of the polypeptides given in the  
 XX specification, a method for identifying a compound useful in treating  
 XX pain and a pharmaceutical composition comprising the one or more  
 XX polypeptides or their antibodies. The polynucleotide or the compound that  
 XX modulates its activity is useful for preparing a medicament for treating  
 XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 XX therapy). The sequence presented is a rat protein (shown in Table 2 of  
 XX the specification) which is differentially expressed during pain. Note:  
 XX The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic form directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 331 AA;

Query Match 60.5%; Score 46; DB 7; Length 331;  
 Best Local Similarity 63.6%; Pred. No. 64;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFYGGHPGPDY 12  
 Db 298 GYVGPGGYDY 308

RESULT 6  
 ADO19157  
 ID ADO19157 standard; protein; 331 AA.  
 XX  
 XX AC ADO19157;  
 XX

XX 12-AUG-2004 (first entry)  
 XX  
 XX Human PRO polypeptide #46.  
 DE

XX Human; PRO; immune related disorder; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;  
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
 KW diabetes mellitus; renal disease; demyelinating disease;  
 KW central nervous system; peripheral nervous system;  
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW chronic inflammatory demyelinating polyneuropathy.  
 XX

OS Homo sapiens.

PN WO2004043361-A2.

PD 27-MAY-2004.

PF 06-NOV-2003; 2003WO-US035268.

PR 08-NOV-2002; 2002US-0425235P.

XX (GENTH ) GEMENTECH INC.

XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PW,  
 XX Wood WI, Wu TD;  
 PI

XX MPI; 2004-42067/39.

XX N-PSDB; ADO19156.

XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO68398 useful for  
 XX treating an immune related disorder such as systemic lupus erythematosus,  
 XX rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
 XX spondyloarthritis.  
 PT

XX Claim 7; SEQ ID NO 92; 1731pp; English.

XX The invention relates to human PRO polypeptides and the polynucleotides  
 XX encoding them. The polypeptides and polynucleotides are useful for  
 XX treating and diagnosing immune related disorders in mammals. The immune  
 XX related disorders include systemic lupus erythematosus, rheumatoid  
 XX arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 XX sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 XX haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 XX mellitus, immune-mediated renal disease, demyelinating diseases of the  
 XX central or peripheral nervous system, demyelinating polyneuropathy,  
 XX Guillain-Barre syndrome and chronic inflammatory demyelinating  
 XX polyneuropathy. This sequence represents a human PRO polypeptide of the  
 XX invention.  
 CC

SO Sequence 331 AA;

Query Match 60.5%; Score 46; DB 8; Length 331;  
 Best Local Similarity 63.6%; Pred. No. 64;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFYGGHPGPDY 12  
 Db 298 GYVGPGGYDY 308

RESULT 7  
 ADP54207  
 ID ADP54207 standard; protein; 331 AA.  
 XX  
 XX AC ADP54207;  
 XX  
 XX DT 18-NOV-2004 (first entry)  
 XX  
 XX DE Human PRO protein sequence SEQ ID NO:183.  
 XX



KW human; PRO; immune related disease; inflammatory immune response;  
 KW immune response stimulation; anti-allergic; antianemic; antiarthritic;  
 KW antiaesthetic; antidiabetic; antiinflammatory; antiparietal;  
 KW antirheumatic; antihypertensive; CNS; dermatological; gastroenteric;  
 KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
 KW virucide; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004039956-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 28-OCT-2003; 2003WO-US034381.  
 XX  
 PR 29-OCT-2002; 2002US-0422472P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
 PI Wood WI, Wu TD;  
 XX  
 DR WPI; 2004-376182/35.  
 DR N-PSDB; ADP54206.  
 XX  
 PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing  
 PT and treating an immune related disease, e.g. systemic lupus  
 PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
 PT stimulating an immune response.  
 XX  
 PS Claim 1; SEQ ID NO 183; 3009PP; English.  
 XX  
 CC The present invention describes an isolated PRO nucleic acid (1). Also  
 CC described: (1) a vector comprising (1); (2) a host cell comprising the  
 CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
 CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
 CC antibody which specifically binds to a polypeptide of (4); (7) a  
 CC composition of matter comprising a polypeptide of (4); an agonist or  
 CC antagonist of the polypeptide or an antibody that binds to the  
 CC polypeptide in combination with a carrier; (8) an article of manufacture  
 CC comprising a container, a label on the container and a composition of  
 CC matter of (7); (9) a method of treating an immune related disease in a  
 CC mammal; (10) a method for determining the presence of a PRO polypeptide  
 CC in a sample suspected of having the polypeptide; (11) a method of  
 CC diagnosing an immune related disease or an inflammatory immune response  
 CC in mammal; (12) a method of identifying a compound that inhibits or  
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide  
 CC; and (13) a method of stimulating the immune response in a mammal. The  
 CC PRO sequences have anti-allergic, antianemic, antiarthritic,  
 CC antiaesthetic, antidiabetic, antiinflammatory, antiparietal,  
 CC antirheumatic, antihypertensive, CNS, dermatological, gastroenteric,  
 CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,  
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
 CC virucide activities, and can be used in gene therapy. The nucleic acid  
 CC (1) and the encoded polypeptides, compositions, kits and methods are  
 CC useful in diagnosing and treating an immune related disease and in  
 CC stimulating an immune response. The present sequence represents a human  
 CC PRO protein from the present invention.  
 XX  
 SQ Sequence 331 AA;  
 QY Query Match 60.5%; Score 46; DB 8; Length 331;  
 Db Best Local Similarity 63.6%; Pred. No. 64;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 2 GFYGHGPFY 12  
 298 GYGYGPFY 308  
 RESULT 8

ADP23166  
 ID ADP23166 standard; protein; 331 AA.  
 AC ADP23166;  
 DT 18-NOV-2004 (first entry)  
 DE PRO polypeptide SEQ ID NO:260.  
 KW PRO; antiinflammatory; antirheumatic; antiparietal; immunosuppressive;  
 KW osteopathic; antidiabetic; dermatological; antiparietal; antiallergic;  
 KW antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2004041170-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034312.  
 XX  
 PR 01-NOV-2002; 2002US-0423394P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Clark H, Schoenfeld J, Van Lookeren W, Williams PM, Wood WI;  
 PI Wu TD;  
 XX  
 DR WPI; 2004-419628/39.  
 DR N-PSDB; ADP23165.  
 XX  
 PT New PRO polypeptides and polynucleotides, useful for treating e.g.  
 PT erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated  
 PT renal disease, or demyelinating diseases of the central or peripheral  
 PT nervous system.  
 XX  
 PS Claim 7; SEQ ID NO 260; 2940PP; English.  
 XX  
 CC The invention relates to a novel isolated nucleic acid and the PRO  
 CC polypeptide encoded by it. A protein of the invention has  
 CC antiinflammatory, antirheumatic, antiparietal, immunosuppressive,  
 CC osteopathic, antidiabetic, dermatological, antiparietal, antiallergic,  
 CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide  
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
 CC agonist, antagonist, or antibody that specifically binds to the  
 CC polypeptide is useful for treating an immune related disorder such as  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease of the central or peripheral nervous  
 CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,  
 CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary  
 CC disease, infectious or autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
 CC hypersensitivity, urticaria, an immunologic disease of the lung,  
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
 CC pneumonitis, a transplantation associated disease, graft rejection or  
 CC graft-versus-host disease. The present sequence represents a PRO protein  
 CC of the invention.  
 XX  
 SQ Sequence 331 AA;  
 QY Query Match 60.5%; Score 46; DB 8; Length 331;  
 Db Best Local Similarity 63.6%; Pred. No. 64;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 2 GFYGHGPFY 12

Db	298	GYGCGPGFDY 308	: :    : :
RESULT 9			
ABP69582	ID	ABP69582 standard; protein; 332 AA.	
XX	ABP69582;		
XX	20-JAN-2003	(first entry)	
XX	Human polypeptide SEQ	ID NO 1629.	
XX	Human; genome mapping; gene therapy; food supplement; virus; fungus;		
KW	cell-proliferative disorder; neurodegenerative diseases; bacterial;		
KW	Parkinson's disease; Alzheimer's disease; autoimmune disease;		
KW	multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;		
KW	arthritis; cytostatic; immunomodulator; nocotropic; neuroprotective;		
KW	antiparkinsonian; antidiabetic; immunosuppressive; dermatological;		
KW	haemostatic; vulnereary; fungicide; antibacterial; virucide; protozoacide;		
KW	antiarthritic.		
XX	Homo sapiens.		
XX	WO200270539-A2.		
XX	12-SEP-2002.		
XX	05-MAR-2002; 2002WO-US005095.		
XX	05-MAR-2001; 2001US-00799451.		
XX	(HYSE-) HYSEQ INC.		
XX	Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;		
PI	Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;		
PI	Wehrman T, Wang J, Wang D, Drmanac RT;		
DR	WPI: 2002-759812/82.		
DR	N-PSDB: ABZ11799.		
PT	New polynucleotides comprising sequences assembled from expressed		
PT	sequence tags (ESTs), useful for treating cell-proliferative,		
PT	neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet		
PT	or coagulation disorders.		
XX	Claim 9; SEQ ID NO 1629; 1012pp + Sequence Listing; English.		
XX	The invention relates to an isolated polynucleotide (I) comprising a		
CC	nucleotide sequence selected from any of 948 sequences (ABZ1119-		
CC	ABZ12066) or their mature protein coding portion, active domain coding		
CC	protein or complementary sequences. The polynucleotides are useful for		
CC	identifying expressed genes or for physical mapping of human genome. The		
CC	encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight		
CC	markers, as a food supplement, for generating antibodies, in medical		
CC	imaging, screening and diagnostic assays and for treating cell-		
CC	proliferative disorders (cancer), neurodegenerative diseases (Parkinson's		
CC	or Alzheimer's disease), autoimmune diseases (multiple sclerosis,		
CC	diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,		
CC	platelet or coagulation disorders, wound, burns, incision, ulcers, liver		
CC	or lung fibrosis, infections (bacterial, viral, fungal, parasitic),		
CC	arthritis, etc. Note: The sequence data for this patent did not form part		
CC	of the printed specification, but was obtained in electronic format		
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences		
XX	Sequence 332 AA;		
XX	Query March 60 5%; Score 46; DB 5; Length 332;		
XX	Best Local Similarity 63.6%; Pred. No. 64;		
XX	Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;		
XX	2 GYGCGPGFDY 12		

DB		299	GYYGGEYDY	309
	: :	: :	: :	: :
RESULT 10				
ADG77005	ID	ADG77005	standard; protein; 332 AA.	
XX	AC	ADG77005;		
XX	DT	11-MAR-2004	(first entry)	
XX	DE	Human nucleic acid associated polypeptide (NAP) 33.		
XX	KW	nucleic acid associated polypeptide; NAP; cytosolic;		
XX	KW	antiartherosclerotic; anticoagulant; neurotropic; neuroprotective;		
XX	KW	cerebroprotective; anti-HIV; antiallergic; antiinflammatory;		
XX	KW	thyromimetic; gene therapy; cell proliferative; cancer; atherosclerosis;		
XX	KW	neurological; epilepsy; Huntington's disease; stroke; immune;		
XX	KW	inflammatory; AIDS; allergy; developmental; Hypothyroidism;		
XX	Cushing's syndrome; infection; human.			
OS	Homo sapiens.			
EN	WO2003076586-A2.			
XX	PD	18-SEP-2003.		
XX	PF	05-MAR-2003; 2003WO-US007002.		
XX	PR	06-MAR-2002; 2002US-0362329P.		
XX	PR	15-MAR-2002; 2002US-0364438P.		
XX	PR	19-APR-2002; 2002US-0373891P.		
PA	(INCYTE GENOMICS INC.			
P1	Richardson TW, Elliott VS, Sprague WM, Jiang X, Tang YT;			
P1	Zebaryadjan Y, Baughn MR, Jackson AA, Kable AE, Lee EA, Khan FA,			
P1	Yue H, Forsythe JD, Ramkumar J, Griffin JA, Li JJ, Margulis JP,			
P1	Lehr-Watson PM, Jin P, Hawkins PR, Wilson AD, Swarnakar A, He A;			
P1	Hafalla AA, Tran B, Duggan BM, Emerling BM, Borowsky ML, Yao MG;			
P1	Chawla NK, Burford N, Khare R, Lee S, Becha SD, Lee SY;			
XX	WP1; 2003-756814/71.			
DR	N-PSDB; ADG77058.			
PT	New human nucleic acid associated proteins (NAP), useful for diagnosing,			
PT	treating and preventing diseases or conditions associated with the			
PT	aberrant NAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or			
PT	infections.			
XX				
XX				
PS	Claim 1; SEQ ID NO 33; 373bp; English.			
XX				
CC	This invention relates to a novel isolated human nucleic acid associated			
CC	polypeptide (NAP). The invention may be useful for the development of			
CC	compounds with a cytostatic, antiatherosclerotic, anticoagulant,			
CC	neotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,			
CC	antiinflammatory or thyromimetic activity and also for gene therapy. The			
CC	invention may prove useful for the development of treatments for diseases			
CC	or conditions associated with the decreased expression or overexpression			
CC	of NAP, such as cell proliferative (for example cancer,			
CC	atherosclerosis), neurological (for example epilepsy, Huntington's			
CC	disease, stroke), immune/inflammatory (for example AIDS, allergies) and			
CC	developmental (for example Hypothyroidism, Cushing's syndrome) disorders,			
CC	or infections. The present sequence is that of a human NAP protein of			
CC	the invention.			
XX				
XX				
SEQ	Sequence 332 AA:			
Query Match	60.5%; Score 46; DB 7; Length 332;			
Best Local Similarity	63.6%; Pred. No. 64;			
Matches 7; Conservative	2; Mismatches 2; Indels 0; Gaps 0;			

Qy 2 GFYGGHPGPDY 12  
|:|:| |:  
Db 299 GYVGPGPDY 309

RESULT 11  
ADM05821  
ID ADM05821 standard; protein; 332 AA.  
XX  
XX ADM05821;  
AC  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Human protein of the invention SEQ ID NO:4506.  
DE  
XX human; gene therapy; diagnostic marker; pharmaceutical.  
KW  
XX Homo sapiens.  
OS  
XX EPI347046-A1.  
PN  
XX 24-SEP-2003.  
PD  
XX 12-APR-2002; 2002EP-00008400.  
PE  
XX 22-MAR-2002; 2002JP-00137785.  
PR  
XX (REAS-) RBS ASSOC BIOTECHNOLOGY.  
PA  
XX Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-723556/69.  
DR N-PSDB; ADM03378.  
XX  
XX New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.  
XX  
XX Claim 1; SEQ ID NO 4506; 305BP; English.  
XX  
XX The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC protein sequence of the invention.  
XX  
SQ Sequence 332 AA;

Query Match 60.5%; Score 46; DB 7; Length 332;  
Best Local Similarity 63.6%; Pred. No. 64;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GFYGGHPGPDY 12  
|:|:| |:  
Db 299 GYVGPGPDY 309

RESULT 12  
AD126203  
ID AD126203 standard; protein; 332 AA.  
XX  
XX AD126203;  
AC  
XX 22-APR-2004 (first entry)  
DT  
XX Human protein that promotes STAT6 activation #84.  
XX

XX human; signal transducer and activator of transcription 6; STAT6;  
KW immunogen; STAT6 activation; allergy; inflammation; autoimmune disease;  
KW diabetes; hyperlipidaemia; infection; cancer; Th1 hyperactive disease;  
KW rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus;  
KW sepsis; asthma; allergic rhinitis; ischemic heart disease;  
KW subarachnoid haemorrhage; viral hepatitis; AIDS.  
XX  
XX Homo sapiens.  
OS  
XX WO2003104277-A2.  
PN  
XX 18-DEC-2003.  
PD  
XX 05-JUN-2003; 2003WO-JP007123.  
PE  
XX 05-JUN-2002; 2002JP-0164257.  
PR 06-JUN-2002; 2002US-0385912P.  
PR 26-DEC-2002; 2002JP-00377326.  
PR 27-DEC-2002; 2002US-0436467P.  
PR 15-MAY-2003; 2003JP-00137505.  
PR 16-MAY-2003; 2003US-0470836P.  
XX  
XX (ASAH ) ASAMI KASEI KK.  
PA  
XX Sugahara T, Matsuda A, Honda G, Muramatsu S, Ishizawa K;  
PI WPI; 2004-122214/12.  
DR N-PSDB; AD126202.  
XX  
XX New signal transducer and activator of transcription 6 activation  
PT promoting purified protein, for diagnosing and treating disease  
PT associated with activation/inhibition of transcription factor e.g.  
PT diabetes and cancer.  
XX  
XX Claim 1; SEQ ID NO 168; 1368BP; English.  
XX  
XX The invention relates to a purified protein promoting signal transducer  
CC and activator of transcription 6 activation (STAT6). The protein is  
CC useful for producing an antibody, which involves administering the  
CC protein or its epitope-bearing fragments to a non-human animal as an  
CC antigen. The nucleic acid is useful for diagnosing a disease or  
CC susceptibility to a disease related to expression or activity of the  
CC protein. A transformant expressing the protein is useful for screening  
CC compounds which inhibit or promote STAT6 activation. A transformant  
CC expressing the protein is useful for producing a pharmaceutical  
CC composition. Compositions, antibodies and antisense molecules are useful  
CC for the treating a disease associated with STAT6 activation such as  
CC allergic diseases, inflammation, autoimmune diseases, diabetes,  
CC hyperlipidaemia, infectious disease and cancers. Compositions are useful  
CC for treating disease associated with STAT6 activation and/or prevention  
CC of Th1 hyperactive diseases. Compositions are also useful in rheumatoid  
CC arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma,  
CC allergic rhinitis, ischemic heart diseases, subarachnoid haemorrhage,  
CC viral hepatitis and AIDS. The protein has efficiently promoting STAT6  
CC activity. The protein or nucleic acid is effectively useful for screening  
CC compounds for treating and preventing disease associated with excessive  
CC activation or inhibition of STAT6. The present sequence represents the  
CC amino acid sequence of a human protein which promotes STAT6 activation.  
XX  
SQ Sequence 332 AA;

Query Match 60.5%; Score 46; DB 8; Length 332;  
Best Local Similarity 63.6%; Pred. No. 64;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GFYGGHPGPDY 12  
|:|:| |:  
Db 299 GYVGPGPDY 309

RESULT 13  
ABG18425

ID ABG18425 standard; protein; 336 AA.  
 XX  
 AC ABG18425;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #18416.  
 XX  
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX food supplement; medical imaging; diagnostic; genetic disorder.  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 XX  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 PI WPI; 2001-639362/73.  
 XX  
 DR N-PSDB; AAS62612.  
 XX  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensic; gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 PS  
 PS Claim 20; SEQ ID NO 48784; 103bp; English.  
 XX  
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensic; gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 336 AA;

Query Match 60.5%; Score 46; DB 4; Length 336;  
 Best Local Similarity 63.6%; Pred. No. 65;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GRYGHPGPDY 12  
 |:|:|:|:|:  
 DB 303 GYGGYGPYDY 313

RESULT 14  
 AB081995  
 ID AB081995 standard; protein; 701 AA.  
 XX

AC AB081995;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Pseudomonas aeruginosa polypeptide #14170.  
 XX  
 KM Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
 XX  
 OS Pseudomonas aeruginosa.  
 XX  
 PN US6551795-B1.  
 XX  
 PD 22-APR-2003.  
 XX  
 PF 18-FEB-1999; 99US-00252991.  
 XX  
 PR 18-FEB-1998; 98US-0074786P.  
 XX  
 PR 27-JUL-1998; 98US-0094190P.  
 XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
 XX  
 PI WPI; 2003-615309/58.  
 XX  
 DR N-PSDB; ABD15566.  
 XX  
 XX  
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.  
 PS  
 PS Disclosure; SEQ ID NO 30741; 455bp; English.  
 XX  
 XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biopchip technology. Sequences AB067826-  
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 701 AA;

Query Match 60.5%; Score 46; DB 7; Length 701;  
 Best Local Similarity 72.7%; Pred. No. 1,4e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGRYGHGPGPD 11  
 |||||:  
 DB 43 EGRRGHGPGRD 53

RESULT 15  
 ADP22190  
 ID ADP22190 standard; protein; 121 AA.  
 XX

AC ADP22190;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX

DE Human anti-TNFA antibody light chain variable region SEQ ID NO:96.  
 XX  
 DE human; monoclonal antibody; tumour necrosis factor- $\alpha$ ; TNFA;  
 KM anti-TNFA antibody; anabolic; antiarteriosclerotic; antiatheritic;  
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 XX

KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
KW neuroprotective; vasotropic; antiapoptotic; TNF $\alpha$  antagonist;  
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KW prostate cancer; immuno-mediated inflammatory disease;  
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KW septic shock; cachexia; anorexia; multiple sclerosis.  
XX  
XX Homo sapiens.  
XX  
XX WO2004050683-A2.  
XX  
XX 17-JUN-2004.  
XX  
XX 02-DEC-2003; 2003WO-US038281.  
XX  
XX 02-DEC-2002; 2002US-0430729P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
XX Haak-Frendsch M, Rathanaswami P, Pigott C, Liang ML, Lee R;  
XX Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
XX  
XX WPI: 2004-480601/45.  
XX N-PSDB; ADP22189.  
XX  
XX New recombinant human monoclonal antibody that specifically binds to  
XX Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
XX as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
XX arthritis.  
XX  
XX Example 10; SEQ ID NO 96; 213pp; English.  
XX  
XX The present invention describes a human monoclonal antibody (I) that  
XX specifically binds to tumour necrosis factor-alpha (TNF $\alpha$ ) and comprises:  
XX (a) a heavy chain complementarity determining region 1 (CDR1) having the  
XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
XX and (b) a light chain CDR1 having the two fully defined 11 amino acid  
XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
XX (M1) the level of TNF $\alpha$  in a patient sample, comprising contacting with  
XX (I), and detecting the level of binding between the antibody and TNF $\alpha$  in  
XX the sample; (2) a composition comprising the antibody or its functional  
XX fragment and a carrier; (3) treating (M2) an animal suffering from a  
XX neoplastic, or an immuno-mediated inflammatory disease by selecting an  
XX animal in need of treatment for the disease by administering the human  
XX monoclonal antibody of (I); and (4) inhibiting (M3) TNF $\alpha$  induced  
XX apoptosis in an animal by selecting an animal in need of treatment for  
XX TNF $\alpha$  induced apoptosis by administering the human monoclonal antibody of  
XX (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
XX antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
XX disorders, immunomodulator, immunosuppressive, nephrotropic,  
XX neuroprotective, vasotropic and antiapoptotic activities, and can be used  
XX as a TNF $\alpha$  antagonist. The antibody (I) is useful in the preparation of  
XX medicament for treating TNF induced apoptosis, neoplastic disease such as  
XX breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
XX stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
XX pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
XX diseases such as rheumatoid arthritis, glomerulonephritis,  
XX atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
XX disease, graft-host reactions, septic shock, cachexia, anorexia, and  
XX multiple sclerosis. The present sequence represents a human anti-TNF $\alpha$   
XX antibody light chain variable region, which is used in the  
XX exemplification of the present invention.  
XX  
XX Sequence 121 AA;

Query Match 59.2%; Score 45; DB 8; Length 121;  
Best Local Similarity 66.7%; Pred. No. 34;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGFYGHHPFDY 12  
| | | | |  
Db 99 ESDYGNPFYDY 110  
Search completed: March 1, 2005, 17:36:05  
Job time : 91.7231 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: March 1, 2005, 17:25:39 ; Search time 23.4462 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-17  
Perfect score: 76  
Sequence: 1 EGFYGHGHPFDY 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCUTS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	60.5	701	US-09-252-991A-30741	Sequence 30741, A
2	45	59.2	158	US-09-583-110-3871	Sequence 3871, Ap
3	45	59.2	170	US-09-107-433-3765	Sequence 3765, Ap
4	45	59.2	569	US-09-252-991A-32280	Sequence 32280, A
5	43	56.6	563	US-09-248-796A-17268	Sequence 17268, A
6	43	56.6	1897	US-09-792-024-98	Sequence 98, Appl
7	42	55.3	979	US-08-514-213A-2	Sequence 2, Appl
8	42	55.3	979	US-09-015-399-5	Sequence 5, Appl
9	42	55.3	1003	US-09-949-016-11260	Sequence 11260, A
10	41	53.9	104	US-09-248-796A-24186	Sequence 24186, A
11	41	53.9	341	US-09-248-796A-20848	Sequence 20848, A
12	40	52.6	255	US-09-248-796A-28030	Sequence 28030, A
13	40	52.6	371	US-09-252-991A-18673	Sequence 18673, A
14	40	52.6	819	US-09-252-991A-19569	Sequence 19569, A
15	39.5	52.0	243	US-09-489-039A-8468	Sequence 8468, Ap
16	39	51.3	26	US-08-943-583-5	Sequence 5, Appl
17	39	51.3	26	US-08-943-583-6	Sequence 6, Appl
18	39	51.3	27	US-08-943-583-1	Sequence 1, Appl
19	39	51.3	168	US-09-376-113-5	Sequence 5, Appl
20	39	51.3	175	US-09-376-113-7	Sequence 7, Appl
21	39	51.3	176	US-09-248-796A-18362	Sequence 18362, A
22	39	51.3	261	US-09-248-796A-19568	Sequence 19568, A
23	39	51.3	400	US-09-543-681A-4952	Sequence 4952, Ap
24	39	51.3	465	US-10-028-180-44	Sequence 44, Appl
25	39	51.3	498	US-09-270-767-45042	Sequence 45042, A
26	39	51.3	500	US-08-987-519-1	Sequence 1, Appl
27	39	51.3	556	US-09-252-991A-18923	Sequence 18923, A

28	38.5	50.7	341	4	US-09-540-236-2889	Sequence 2889, Ap
29	38	50.0	12	3	US-08-836-561-36	Sequence 36, Appl
30	38	50.0	12	4	US-09-434-122-36	Sequence 36, Appl
31	38	50.0	21	4	US-09-010-317-22	Sequence 22, Appl
32	38	50.0	132	4	US-09-513-999C-4828	Sequence 4828, Ap
33	38	50.0	132	4	US-09-513-999C-4831	Sequence 4831, Ap
34	38	50.0	140	3	US-08-836-561-23	Sequence 23, Appl
35	38	50.0	140	4	US-09-434-122-33	Sequence 23, Appl
36	38	50.0	180	4	US-09-248-796A-22820	Sequence 22820, A
37	38	50.0	203	4	US-09-252-991A-26436	Sequence 26436, A
38	38	50.0	223	4	US-09-152-060-116	Sequence 116, App
39	38	50.0	245	4	US-09-533-029-44	Sequence 44, Appl
40	38	50.0	272	4	US-09-949-016-9966	Sequence 9966, Ap
41	38	50.0	272	4	US-09-949-016-9967	Sequence 9967, Ap
42	38	50.0	341	4	US-09-248-796A-18805	Sequence 18805, A
43	38	50.0	362	4	US-09-252-991A-26917	Sequence 26917, A
44	38	50.0	455	4	US-09-538-092-123	Sequence 123, App
45	38	50.0	522	1	US-08-639-237-2	Sequence 2, Appl

## ALIGNMENTS

```
RESULT 1
US-09-252-991A-30741
Sequence 30741, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252, 991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30741
LENGTH: 701
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30741

Query Match      60.5%; Score 46; DB 4; Length 701;
Best Local Similarity 72.7%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1 EGFYGHGHPFD 11
Db      43 EGLRGHGPDT 53

RESULT 2
US-09-583-110-3871
Sequence 3871, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stream et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
FILE REFERENCE: PATHOD-07A
CURRENT APPLICATION NUMBER: US/09/583,110
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 3871
```

LENGTH: 158  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-583-110-3871

Query Match 59.2%; Score 45; DB 4; Length 158;  
Best Local Similarity 77.8%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGFD 11  
DB 4 FIGHPGFN 12

RESULT 3  
US-09-107-433-3765  
Sequence 3765, Application US/09107433  
Patent No. 6800744

GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneka

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 893-5007

TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 3765:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...170

SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

Query Match 59.2%; Score 45; DB 4; Length 170;  
Best Local Similarity 77.8%; Pred. No. 21;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGFD 11  
DB 16 FIGHPGFN 24

RESULT 4  
US-09-252-991A-32290  
Sequence 32290, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196,136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32290

LENGTH: 569

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32290

Query Match 59.2%; Score 45; DB 4; Length 569;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGHGPGFD 11  
DB 45 GGHGPGFD 51

RESULT 5  
US-09-248-796A-17268  
Sequence 17268, Application US/09248796A  
Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Kelch Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

FILE REFERENCE: 107196,132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17268

LENGTH: 563

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-17268

Query Match 56.6%; Score 43; DB 4; Length 563;  
Best Local Similarity 87.5%; Pred. No. 1,3e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGF 10  
DB 522 FYGHPGF 529

RESULT 6  
US-09-792-024-98  
Sequence 98, Application US/09792024  
Patent No. 6783985

GENERAL INFORMATION:  
APPLICANT: Roemer, Terry

APPLICANT: Djang, Bo

APPLICANT: Boone, Charles

APPLICANT: Bussey, Howard



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; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
; FILE OF INVENTION: Targets Discovery
; FILE REFERENCE: 10182-004-999
; CURRENT APPLICATION NUMBER: US/09/792,024
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 490
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 1897
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-792-024-98

Query Match
Best Local Similarity 56.6%; Score 43; DB 4; Length 1897;
Pred. No. 4.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGHPGF 10
Db 1294 FYGHPGF 1301

RESULT 7
; US-08-514-213A-2
; Sequence 2, Application US/08514213A
; Patent No. 6391651
; GENERAL INFORMATION:
; APPLICANT: MacLaren, No. 6391651
; APPLICANT: Lan, Michael
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION AND
; FILE REFERENCE: 14014,0199
; CURRENT APPLICATION NUMBER: US/08/514,213A
; CURRENT FILING DATE: 1995-08-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. 6391651e =
; US-08-514-213A-2

Query Match
Best Local Similarity 55.3%; Score 42; DB 3; Length 979;
Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EGFYGHGPFY 12
Db 250 KGFDPHGHY 261

RESULT 8
; US-09-015-399-5
; Sequence 5, Application US/09015399
; Patent No. 6770460
; GENERAL INFORMATION:
; APPLICANT: Hinkkanen, Ari
; TITLE OF INVENTION: A New Fusion Protein and Its Use in an
; FILE OF INVENTION: Immunoassay for the Simultaneous Detection of
; TITLE OF INVENTION: Autoantibodies Related to Insulin-Dependent Diabetes
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street N.W., Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,399
; FILING DATE: 29-JAN-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-015-399-5

Query Match
Best Local Similarity 55.3%; Score 42; DB 4; Length 979;
Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EGFYGHGPFY 12
Db 250 KGFDPHGHY 261

RESULT 9
; US-09-949-016-11260
; Sequence 11260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11260
; LENGTH: 1003
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11260

Query Match
Best Local Similarity 55.3%; Score 42; DB 4; Length 1003;
Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EGFYGHGPFY 12
Db 274 KGFDPHGHY 285

RESULT 10
; US-09-248-796A-24186
; Sequence 24186, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
```

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; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24186
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-24186

Query Match      53.9%; Score 41; DB 4; Length 104;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 0; Gaps 0; Indels 0;

QY      5 GGHGPGD 11
Db      47 GGHGPGD 53

RESULT 11
US-09-248-796A-20848
; Sequence 20848; Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20848
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-20848

Query Match      53.9%; Score 41; DB 4; Length 341;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 GFGYGHGPGD 11
Db      189 GFGYGHGPGD 198

RESULT 12
US-09-248-796A-28030
; Sequence 28030; Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
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; SEQ ID NO 28030
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-28030

Query Match      52.6%; Score 40; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY      4 YGSHPG 9
Db      48 YGSHPG 53

RESULT 13
US-09-252-991A-18673
; Sequence 18673; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18673
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-18673

Query Match      52.6%; Score 40; DB 4; Length 371;
Best Local Similarity 70.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GFGYGHGPGD 11
Db      87 GAGGAGHGP 96

RESULT 14
US-09-252-991A-19569
; Sequence 19569; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19569
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-19569

Query Match      52.6%; Score 40; DB 4; Length 819;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 EGFGYGHGPG 9
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Db 62 QGLVGCHPG 70

RESULT 15

US-09-489-039A-8468

; Sequence 8468, Application US/09489039A  
; Patent No. 6610836; Patent No. 6610836  
; GENERAL INFORMATION

APPLICANT: Gary Br

APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID

;	TITLE OF INVENTION:	NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;	TITLE OF INVENTION:	PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

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; FILE REFERENCE: 2/09.2004001
; CURRENT APPLICATION NUMBER: U

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CURRENT AFFIDAVIT NUMBER: 05/09/489,039A  
CURRENT FILING DATE: 2000-01-27

; CURREN1 FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 8468

; LENGTH: 243

TYPE: PRT

ORGANISM: K1

US-09-489-039A-8468

### Discussion

Query Match	52.0%;	Score 39.5;	DB 4;	Length 243;
Best Local Similarity	66.7%;	Pred. No. 1.8e+02;		

Matches 8; Conservative 1; Mismatches 2

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

QY 2 GFGGHPG-FDY 12

11

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Job time : 24.4462 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 64.2462 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-17

Perfect score: 76

Sequence: 1 EGFYGHGPGFDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 32804528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*

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17: /cgn2\_6/ptodata/1/pubppaa/US91\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubppaa/US90\_PUBCOMB.pep:\*

19: /cgn2\_6/ptodata/1/pubppaa/US89\_PUBCOMB.pep:\*

20: /cgn2\_6/ptodata/1/pubppaa/US88\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	12	US-10-071-962-17	Sequence 17, App1
2	48	63.2	793	US-10-437-963-171397	Sequence 171397, A
3	47	61.8	597	US-10-425-114-58080	Sequence 58080, A
4	46	60.5	332	US-10-108-260A-4506	Sequence 4506, Ap
5	45	59.2	944	US-10-213-990-27	Sequence 27, App1
6	44	57.9	47	US-10-178-213-411	Sequence 411, App1
7	44	57.9	77	US-10-178-213-410	Sequence 410, App
8	44	57.9	458	US-10-282-122A-50265	Sequence 50265, A
9	43	56.6	122	US-10-424-599-277486	Sequence 277486, A
10	43	56.6	264	US-10-437-963-135092	Sequence 135092, A
11	43	56.6	392	US-10-437-963-164638	Sequence 164638, A
12	43	56.6	1583	US-10-389-566-1672	Sequence 1672, Ap
13	43	56.6	1724	US-10-389-566-2159	Sequence 2159, Ap

14	43	56.6	1897	US-10-032-585-7040	Sequence 7040, Ap
15	42	55.3	176	US-10-767-701-39418	Sequence 39418, A
16	42	55.3	144	US-10-424-599-177869	Sequence 177869, A
17	42	55.3	277	US-10-437-963-114358	Sequence 114358, A
18	42	55.3	979	US-10-038-686-3	Sequence 3, App1
19	41	53.9	123	US-10-424-599-150308	Sequence 150308, A
20	41	53.9	146	US-10-424-599-181333	Sequence 181333, A
21	41	53.9	166	US-10-424-599-277458	Sequence 277458, A
22	41	53.9	215	US-10-425-114-68305	Sequence 68305, A
23	41	53.9	313	US-09-928-457-44	Sequence 44, App1
24	41	53.9	478	US-10-425-114-58912	Sequence 58912, A
25	41	53.9	480	US-10-425-114-61022	Sequence 61022, A
26	41	53.9	592	US-10-032-585-7908	Sequence 7908, Ap
27	40.5	53.3	580	US-10-437-963-141380	Sequence 141380, Ap
28	40	52.6	429	US-10-340-578-10	Sequence 10, App1
29	40	52.6	187	US-10-180-375-200	Sequence 200, App
30	40	52.6	187	US-10-183-687-416	Sequence 416, App
31	40	52.6	187	US-10-399-883-34	Sequence 34, App1
32	40	52.6	190	US-10-286-264-14	Sequence 14, App1
33	40	52.6	190	US-10-325-068-134	Sequence 134, App
34	40	52.6	190	US-10-374-780A-90	Sequence 90, App
35	40	52.6	190	US-10-412-699B-306	Sequence 306, App
36	40	52.6	321	US-10-437-963-107505	Sequence 107505, A
37	40	52.6	431	US-10-062-254-272	Sequence 272, App
38	40	52.6	440	US-10-424-599-219391	Sequence 219391, A
39	40	52.6	455	US-09-738-626-6527	Sequence 6527, Ap
40	40	52.6	455	US-10-494-541-36	Sequence 36, App1
41	40	52.6	456	US-10-425-114-64327	Sequence 64327, A
42	40	52.6	616	US-10-322-281-26	Sequence 26, App1
43	40	52.6	712	US-10-128-714-3108	Sequence 3108, Ap
44	40	52.6	716	US-10-128-714-8108	Sequence 8108, Ap
45	39.5	52.0	56	US-10-437-963-119540	Sequence 119540, A

## ALIGNMENTS

RESULT 1

US-10-071-962-17

Sequence 17, Application US/10071962

Publication No. US20030170237A1

GENERAL INFORMATION:

APPLICANT: Baifu Ni

APPLICANT: Bill N.C. Sun

TITLE OF INVENTION: G-GSP Receptor Agonist Antibodies and

FILE REFERENCE: 98-3

CURRENT APPLICATION NUMBER: US/09/303,155A

PRIOR FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US/09/303,155A

PRIOR FILING DATE: 1999-04-30

PRIOR APPLICATION NUMBER: 60/083,575

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 12

TYPE: PRT

ORGANISM: mouse

US-10-071-962-17

Query Match 100.0%; Score 76; DB 14; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.9e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EGFYGHGPGFDY 12

1 EGFYGHGPGFDY 12

RESULT 2

US-10-437-963-171397

Sequence 171397, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 171397  
LENGTH: 793  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_69633C.1.pep  
US-10-437-963-171397

Query Match 63.2%; Score 48; DB 16; Length 793;  
Best Local Similarity 63.6%; Pred. No. 54;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EGYGHPGPD 11  
Db 171 DGIYAGHPSPD 181

RESULT 3  
US-10-425-114-58080  
Sequence 58080, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53113)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73126  
SEQ ID NO 58080  
LENGTH: 597  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: 701001844\_FLI.pep  
US-10-425-114-58080

Query Match 61.8%; Score 47; DB 15; Length 597;  
Best Local Similarity 87.5%; Pred. No. 58;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GFGYGHG 9  
Db 122 GFGYGHG 129

RESULT 4  
US-10-108-260A-4506  
Sequence 4506, Application US/10108260A  
Publication No. US20040005560A1  
GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: NO. US20040005560A1 full length cDNA  
FILE REFERENCE: H1-A0106  
CURRENT APPLICATION NUMBER: US/10/108,260A  
NUMBER OF SEQ ID NOS: 5458  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4506  
LENGTH: 332  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-108-260A-4506

Query Match 60.5%; Score 46; DB 15; Length 332;  
Best Local Similarity 63.6%; Pred. No. 46;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGYGHGPDY 12  
Db 299 GYGYGPGYDY 309

RESULT 5  
US-10-213-990-27  
Sequence 27, Application US/10213990  
Publication No. US20030082595A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Bo  
APPLICANT: Bussey, Howard  
APPLICANT: Storms, Reg  
APPLICANT: Roemer, Terry  
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL  
TITLE OF INVENTION: ENZYMES AND METHODS OF USE  
FILE REFERENCE: 10182-019-999  
CURRENT APPLICATION NUMBER: US/10/213,990  
CURRENT FILING DATE: 2002-08-05  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 27  
LENGTH: 944  
TYPE: PRT  
ORGANISM: Aspergillus  
US-10-213-990-27

Query Match 59.2%; Score 45; DB 14; Length 944;  
Best Local Similarity 54.5%; Pred. No. 1,9e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGYGHGPDY 12  
Db 355 GYGYGTSYDY 365

RESULT 6  
US-10-178-213-411  
Sequence 411, Application US/10178213  
Publication No. US20030041348A1  
GENERAL INFORMATION:  
APPLICANT: Simmons, Carl R.  
APPLICANT: Navarro Acevedo, Pedro A.  
APPLICANT: Harvell, Leslie  
APPLICANT: Cahoon, Rebecca  
APPLICANT: McCutchen, Billy Fred  
APPLICANT: Lu, Albert  
APPLICANT: Hertmann, Rafael  
APPLICANT: Wong, James  
TITLE OF INVENTION: Defensin Polynucleotides and Methods of  
TITLE OF INVENTION: Use  
FILE REFERENCE: 35718/246703  
CURRENT APPLICATION NUMBER: US/10/178,213  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: 60/300,152  
PRIOR FILING DATE: 2001-06-22

```

; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 411
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Tropaeolum majus
US-10-178-213-411
```

```

Query Match      57.9%; Score 44; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EGFYGGH 7
        |||||
Db      27 EGFYGGH 33
```

## RESULT 7

```

US-10-178-213-410
; Sequence 410, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McClutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Hermann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Tropaeolum majus
US-10-178-213-410
```

```

Query Match      57.9%; Score 44; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 EGFYGGH 7
        |||||
Db      57 EGFYGGH 63
```

## RESULT 8

```

US-10-282-122A-50266
; Sequence 50266, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
```

```

; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA, 03A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50266
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-10-282-122A-50266
```

```

Query Match      57.9%; Score 44; DB 15; Length 458;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 EGFYGGHPGD 11
        :|||:
Db      381 QGFYAKHPGD 391
```

## RESULT 9

```

US-10-424-599-277486
; Sequence 277486, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 277486
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_92593C.1.pep
US-10-424-599-277486
```

```

Query Match      56.6%; Score 43; DB 15; Length 122;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 FYGGHPGD 11
        :|||:
Db      3 FYGGHPGD 11
```

Db 87 YGCGHGF 95

RESULT 10

US-10-437-963-135092  
; Sequence 135092, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Bred  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ. ID NOS: 204966  
; SEQ. ID NO 135092  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_36800C.1.pep  
US-10-437-963-135092

Query Match 56.6%; Score 43; DB 16; Length 264;  
Best Local Similarity 87.5%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYGGHGF 9  
Db 171 GYGGHGF 178

RESULT 11

US-10-437-963-164638  
; Sequence 164638, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Bred  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ. ID NOS: 204966  
; SEQ. ID NO 164638  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_63517C.1.pep  
US-10-437-963-164638

Query Match 56.6%; Score 43; DB 16; Length 392;  
Best Local Similarity 70.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYGGHGF 11  
Db 360 GYGGHGF 369

RESULT 12

US-10-389-566-1672  
; Sequence 1672, Application US/10389566  
; Publication No. US20040025202A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology, LLC  
; APPLICANT: Laurie, Cathy C  
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants  
; FILE REFERENCE: 38-77(52900)D  
; CURRENT APPLICATION NUMBER: US/10/389,566  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/365,301  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/391,786  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/392,018  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ. ID NOS: 2459  
; SOFTWARE: PatentIn version 3.2  
; SEQ. ID NO 1672  
; LENGTH: 1583  
; TYPE: PRT  
; ORGANISM: Cryptococcus neoformans  
US-10-389-566-1672

Query Match 56.6%; Score 43; DB 15; Length 1583;  
Best Local Similarity 87.5%; Pred. No. 6.4e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGGHGF 10  
Db 1158 FYGGHGF 1165

RESULT 13

US-10-389-566-2159  
; Sequence 2159, Application US/10389566  
; Publication No. US20040025202A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology, LLC  
; APPLICANT: Laurie, Cathy C  
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants  
; FILE REFERENCE: 38-77(52900)D  
; CURRENT APPLICATION NUMBER: US/10/389,566  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/365,301  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/391,786  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/392,018  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ. ID NOS: 2459  
; SOFTWARE: PatentIn version 3.2  
; SEQ. ID NO 2159  
; LENGTH: 1724  
; TYPE: PRT  
; ORGANISM: Cryptococcus neoformans  
US-10-389-566-2159

Query Match 56.6%; Score 43; DB 15; Length 1724;  
Best Local Similarity 87.5%; Pred. No. 6.9e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FYGGHGF 10  
Db 1182 FYGGHGF 1189

RESULT 14

US-10-032-585-7040  
; Sequence 7040, Application US/10032585



```

; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7040
; LENGTH: 1897
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7040

```

```

Query Match          56.6%; Score 43; DB 14; Length 1897;
Best Local Similarity 87.5%; Pred. No. 7.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      3 FYGHPGR 10
      |||||
Db      1294 FYGHPGR 1301

```

```

RESULT 15
US-10-767-701-39418
; Sequence 39418, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 39418
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C13495_1.pep
US-10-767-701-39418

```

```

Query Match          55.3%; Score 42; DB 16; Length 176;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EGFYGHGPG 9
      |||||
Db      15 KGFHGYGPG 23

```

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Search completed: March 1, 2005, 17:52:50
Job time : 65.2462 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 16.2462 Seconds  
(without alignments)  
71.065 Million cell updates/sec

Title: US-10-071-962-17  
Perfect score: 76  
Sequence: 1 EGFGYGHGPFY 12

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	64.5	378	2	D69793 conserved hypotnet
2	46	60.5	137	2	A03865 hypotnetical prote
3	46	60.5	353	1	S56750 single stranded D
4	44	57.9	760	2	T16726 hypotnetical prote
5	43.5	57.2	174	2	AD2666 conserved hypotnet
6	43.5	57.2	192	2	B97448 immunoreactive 14k
7	42	55.3	153	2	AB2666 conserved hypotnet
8	42	55.3	153	2	A97448 immunoreactive 14k
9	42	55.3	265	2	G87501 hypotnetical prote
10	41	53.9	127	2	B81188 hypotnetical prote
11	41	53.9	140	2	S31686 Ig heavy chain V r
12	41	53.9	167	2	AB2796 acetyltransferase
13	41	53.9	167	2	B97575 hypotnetical prote
14	41	53.9	308	2	T16654 hypotnetical prote
15	41	53.9	322	2	T44427 hypotnetical prote
16	41	53.9	322	2	AB1990 hypotnetical prote
17	41	53.9	917	2	S07183 hypotnetical prote
18	41	53.9	1029	2	PF7369 TonB-dependent rec
19	41	53.9	1374	2	AB3259 extracellular seri
20	40	52.6	73	2	AE0136 keratin, scale (cl
21	40	52.6	78	2	H69905 probable glycine-r
22	40	52.6	127	2	D84469 probable glycine-r
23	40	52.6	390	2	T139570 probable porin (si
24	40	52.6	486	1	KRXL keratin 3, type I,
25	40	52.6	641	2	A55549 glucan 1,6-alpha-1
26	40	52.6	732	2	A86395 hypotnetical prote
27	40	52.6	739	2	A51727 cellulase (EC 3.2.
28	40	52.6	2059	2	T13858 probable DNA-dirc
29	40	52.6	2160	2	T20241 hypotnetical prote

30	39.5	52.0	346	2	T49147 nitrilase (EC 3.5.
31	39.5	52.0	346	2	S22398 nitrilase (EC 3.5.
32	39	51.3	135	2	G84469 probable glycine-r
33	39	51.3	148	2	T18236 protein-tyrosine-p
34	39	51.3	176	1	F64725 probable NAD(P)H2
35	39	51.3	176	2	A90635 probable NAD(P)H o
36	39	51.3	176	2	A85486 probable NAD(P)H o
37	39	51.3	184	2	S77928 exoskeletal protei
38	39	51.3	246	2	AB4977 hypotnetical prote
39	39	51.3	276	2	AD1232 gamma-glutamyl kin
40	39	51.3	276	2	AC1586 gamma-glutamyl kin
41	39	51.3	281	2	E90112 26S proteasome reg
42	39	51.3	306	2	S56259 26S proteasome reg
43	39	51.3	308	2	T43293 multidrug resistan
44	39	51.3	312	2	T33344 hypotnetical prote
45	39	51.3	319	2	S44642 hypotnetical prote

## ALIGNMENTS

```
RESULT 1
D69793
conserved hypotnetical protein yeeK - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: D69793
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Benter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerich, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gall
iech, U.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadle, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetre, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winter, P.; Wipat, A.; Yamamoto, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.P.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69793
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-378 <KUN>
A:Cross-references: UNIPROT:O31510; GB:Z99107; GB:AL009126; NID:G2632866; PIDN:CAB12505.
C/Genetics:
A:Gene: yeeK
Query Match 64.5%; Score 49; DB 2; Length 378;
Best Local Similarity 77.8%; Pred. No. 3.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 GFYGHGPF 10
DB 37 GMYGHPGV 45

RESULT 2
A03865
hypotnetical protein B-137 - human adenovirus 2
C/Species: Mastadenovirus h2 (human adenovirus 2)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: B92351; B92352; A03865
R/Gingeras, T.R.; Sciaky, D.; Gelinas, R.E.; Bing-Dong, J.; Yen, C.E.; Kelly, M.M.; Bull
U. Biol. Chem. 257, 13475-13491, 1982
A>Title: Nucleotide sequences from the adenovirus-2 genome.
A:Reference number: A92351; MUID:83056843; PMID:7142161
A:Accession: B92351
A:Molecule type: DNA
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A;Residues: 1-137 <GIN>  
A;Cross-references: UNIPROT:P03293  
R;A:lestrom, P.; Akusjarvi, G.; Pettersson, M.; Pettersson, U.  
J. Biol. Chem. 257, 13492-13498, 1982  
A;Title: DNA sequence analysis of the region encoding the terminal protein and the hyp  
A;Reference number: A92352; MUID:83056844; PMID:7142162  
A;Accession: E92352  
A;Molecule type: DNA  
A;Residues: 1-137 <ALE>  
C;Superfamily: Mastadenovirus h2 hypothetical protein B-137

Query Match 60.5%; Score 46; DB 2; Length 137;  
Best Local Similarity 54.5%; Pred. No. 3.7;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGFYGGHGF 11  
DB 75 QGYHGGHGF 85

## RESULT 3

single stranded D box binding factor 2 - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: S56750  
R;Smith, M.P.; Rueschen, B.; Snipe, L.; Wijnholds, J.; Ab, G.  
Nucleic Acids Res. 23, 2389-2395, 1995  
A;Title: Cloning and characterization of a nuclear, site specific ssDNA binding protein.  
A;Reference number: S56750; MUID:95357145; PMID:7650716  
A;Accession: S56750  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-353 <SMI>  
C;Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology  
F;91-157/Domain: ribonucleoprotein repeat homology <RKM1>  
F;175-241/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 60.5%; Score 46; DB 1; Length 353;  
Best Local Similarity 63.6%; Pred. No. 9.7;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGYGGHGF 12  
DB 320 GYGGYGGY 330

## RESULT 4

hypothetical protein R12B2.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: T16726  
R;Miller, N.  
submitted to the EMBL Data Library, June 1994  
A;Description: The sequence of C. elegans cosmid R12B2.  
A;Reference number: Z18567  
A;Accession: T16726  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-760 <ML>  
A;Cross-references: EMBL:U00066; NID:9495688; PID:9495693; PIDN:AAA50743.1; CESP:R12B2.5  
C;Experimental source: strain Bristol N2  
C;Genetics:  
A;Gene: CESP:R12B2.5  
A;Introns: 19/2; 94/1; 237/3; 622/3; 728/3

Query Match 57.9%; Score 44; DB 2; Length 760;  
Best Local Similarity 66.7%; Pred. No. 43;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGGHGGFDY 12  
|||||:

DB 451 YGGHGGYGH 459

## RESULT 5

conserved hypothetical protein Atu0730 [imported] - Agrobacterium tumefaciens (strain C5)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AD2666  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavh, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E  
ster, B.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AD2666  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 1-174 <KUR>  
A;Cross-references: UNIPROT:Q8UHF2; GB:AE008688; PIDN:AAL41746.1; PID:G17739097; GSPDB:G  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:

A;Gene: Atu0730  
A;Map position: circular chromosome

Query Match 57.2%; Score 43.5; DB 2; Length 174;  
Best Local Similarity 66.7%; Pred. No. 12;  
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 GFGYGGHGF-DY 12  
DB 69 GWYGGHGRDY 80

## RESULT 6

immunoreactive 14K protein ba14K (U62541) [imported] - Agrobacterium tumefaciens (strain  
B97448  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: B97448  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume  
A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: B97448  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 1-192 <KUR>  
A;Cross-references: UNIPROT:Q8UHF2; GB:AE007869; PIDN:AAK8653.1; PID:G15155699; GSPDB:G  
C;Genetics:  
A;Gene: AGR\_C\_1323  
A;Map position: circular chromosome

Query Match 57.2%; Score 43.5; DB 2; Length 192;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 GFGYGGHGF-DY 12  
DB 87 GWYGGHGRDY 98

## RESULT 7

conserved hypothetical protein Atu0728 [imported] - Agrobacterium tumefaciens (strain C5)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AB2666  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavh, T.; Levy, R.; Li, M.; McClell

Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E. W.  
 A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
 A:Reference number: AB2577; MUID:21608550; PMID:11743193  
 A:Accession: AB2666  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-153 <KUR>  
 A:Cross-references: UNIPROT:Q8UHF4; GB:AE008688; PIRN:AAL1744.1; PID:g17739095; GSPDB:C  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: Atu0728  
 A:Map position: circular chromosome

Query Match 55.3%; Score 42; DB 2; Length 153;  
 Best Local Similarity 60.0%; Pred. No. 18;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EGFYGHGPF 10  
 Db 69 DGFYNGHRY 78

RESULT 8  
 A97448  
 immunoreactive 14K protein balak (U62541) [imported] - *Agrobacterium tumefaciens* (strain C)Species: *Agrobacterium tumefaciens*  
 C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
 C/Accession: A97448  
 R:Goodner, B.; Hinkle, G.; Gatlung, S.; Miller, N.; Blanchard, M.; Gurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* C58.  
 A:Reference number: A97359; MUID:21608551; PMID:11743194  
 A:Accession: A97448  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-153 <KUR>  
 A:Cross-references: UNIPROT:Q8UHF4; GB:AE007869; PIDN:AAK6538.1; PID:g15155698; GSPDB:C  
 C:Genetics:  
 A:Gene: AGR\_C\_1322  
 A:Map position: circular chromosome

Query Match 55.3%; Score 42; DB 2; Length 153;  
 Best Local Similarity 60.0%; Pred. No. 18;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EGFYGHGPF 10  
 Db 69 DGFYNGHRY 78

RESULT 9  
 G87501  
 hypothetical protein CC2036 [imported] - *Caulobacter crescentus*  
 C:Species: *Caulobacter crescentus*  
 C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
 C/Accession: G87501  
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Klotz, P.; Ermlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A>Title: Complete Genome Sequence of *Caulobacter crescentus*.  
 A:Reference number: A87249; MUID:21173698; PMID:11259647  
 A:Accession: G87501  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-265 <STO>  
 A:Cross-references: UNIPROT:Q9A6P8; GB:AE005673; NID:g13423511; PIDN:AAK24011.1; GSPDB:C  
 C:Genetics:  
 A:Gene: CC2036

Query Match 55.3%; Score 42; DB 2; Length 265;  
 Best Local Similarity 77.8%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 FYGHPGPD 11  
 Db 73 FYAGHYGPD 81

RESULT 10  
 B81188  
 hypothetical protein NMB0515 [imported] - *Neisseria meningitidis* (strain MC58 serogroup C)Species: *Neisseria meningitidis*  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C/Accession: B81188  
 R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizze, M. Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter, A.; et al.  
 A>Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
 A:Reference number: A81000; MUID:20175755; PMID:10710307  
 A:Accession: B81188  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-127 <TET>  
 A:Cross-references: UNIPROT:Q9K0R5; GB:AE002408; GB:AE002098; NID:g7225740; PIDN:AAF4094  
 A:Experimental source: serogroup B, strain MC58  
 C:Genetics:  
 A:Gene: NMB0515  
 C:Superfamily: *Neisseria meningitidis* hypothetical protein NMB0515

Query Match 53.9%; Score 41; DB 2; Length 127;  
 Best Local Similarity 63.6%; Pred. No. 21;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GFYGHGPF 12  
 Db 21 GRYGNGGPD 31

RESULT 11  
 S31686  
 Ig heavy chain V region - human (fragment)  
 C:Species: *Homo sapiens* (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S31686  
 R:Cusinieri, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C. submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the A:Reference number: S31585  
 A:Accession: S31686  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-140 <CU>  
 A:Cross-references: EMBL:Z14205; NID:g30969; PIRN:CAA78574.1; PID:g30970  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterocramer; immunoglobulin  
 F/34-117/Domain: immunoglobulin homology <IM>

Query Match 53.9%; Score 41; DB 2; Length 140;  
 Best Local Similarity 70.0%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 FYGHPGPD 12  
 Db 120 FAGGSPSFDY 129

RESULT 12  
 AB2796  
 acetyltransferase [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens  
 C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
 C/Accession: AB2796  
 R/Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
 erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A/Reference number: AB2577; PMID:21608550; PMID:11743193  
 A/Accession: AB2796  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-167 <RUR>  
 A/Cross-references: UNIPROT:Q8UEH2; GB:AE008686; P1DN:AL42784.1; P1D:G17740228; GSPDB:C  
 A/Experimental source: strain C58 (Dupont)  
 C/Genetics:  
 A/Gene: Atul785  
 A/Map position: circular chromosome

Query Match 53.9%; Score 41; DB 2; Length 167;  
 Best Local Similarity 70.0%; Pred. No. 27;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GFGYGHGPGD 11  
 | | | | |  
 154 GIVGFHGPFD 163

RESULT 13  
 B97575  
 hypothetical protein AGR\_C\_3283 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
 C/Accession: B97575  
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qucollo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A/Reference number: A97359; PMID:21608551; PMID:11743194  
 A/Accession: B97575  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-167 <RUR>  
 A/Cross-references: UNIPROT:Q8UEH2; GB:AE007869; P1DN:AK87555.1; P1D:G15156891; GSPDB:C  
 C/Genetics:  
 A/Gene: AGR\_C\_3283  
 A/Map position: circular chromosome

Query Match 53.9%; Score 41; DB 2; Length 167;  
 Best Local Similarity 70.0%; Pred. No. 27;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GFGYGHGPGD 11  
 | | | | |  
 154 GIVGFHGPFD 163

RESULT 14  
 T16654  
 hypothetical protein R02F2.5 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: T16654  
 R/Pauley, A.  
 submitted to the EMBL Data Library, May 1994  
 A/Description: The sequence of C. elegans cosmid R02F2.  
 A/Reference number: Z18555  
 A/Accession: T16654  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-223 <PAU>

A/Cross-references: UNIPROT:Q21648; EMBL:U00055; NID:G485143; P1D:G485148; P1DN:AAA50721.  
 A/Experimental source: strain Bristol N2  
 C/Genetics:  
 A/Gene: CSP:R02F2.5  
 A/Introns: 22/3; 38/3

Query Match 53.9%; Score 41; DB 2; Length 223;  
 Best Local Similarity 61.5%; Pred. No. 37;  
 Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 GFGY-GHGPFD 12  
 | | | | |  
 198 GFGYGYGPGFDR 210

RESULT 15  
 T44427  
 hypothetical protein - fission yeast (Schizosaccharomyces pombe)  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
 C/Accession: T44427  
 R/Shimanuki, M.; Saka, Y.; Yanagida, M.; Toda, T.  
 J. Cell Sci. 108, 569-579, 1995  
 A/Title: A novel essential fission yeast gene pad1+ positively regulates pap1+-dependent  
 A/Reference number: Z22764; PMID:95286704; PMID:7769002  
 A/Accession: T44427  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-308 <SHI>  
 A/Cross-references: UNIPROT:P41878; EMBL:D31731; NID:G497632; P1DN:BA06529.1; P1D:G49763  
 C/Genetics:  
 A/Gene: pad1+

Query Match 53.9%; Score 41; DB 2; Length 308;  
 Best Local Similarity 66.7%; Pred. No. 51;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGYGHGPGF 10  
 | | | | |  
 109 GWYNSHPGF 117

Search completed: March 1, 2005, 17:44:45  
 Job time: 17.2462 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 77.7231 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-17

Perfect score: 76

Sequence: 1 EGFYGHGPFY 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	65.8	340	2	06NYU8
2	50	65.8	340	2	06NYU8
3	49	64.5	63	2	0655W7
4	49	64.5	145	2	031510
5	48	63.2	793	2	07XPR9
6	46	60.5	117	2	08CIR3
7	46	60.5	137	1	Y137_ADE02
8	46	60.5	196	2	07VWV5
9	46	60.5	196	2	07VWV5
10	46	60.5	311	2	07W9K1
11	46	60.5	324	2	07ZYB9
12	46	60.5	326	2	06GM69
13	46	60.5	331	1	ROAA_HUMAN
14	46	60.5	331	2	068311
15	46	60.5	332	2	09QX81
16	46	60.5	506	2	06QAF5
17	45	59.2	297	2	07Q1T9
18	45	59.2	316	2	08B4S3
19	45	59.2	316	2	08KUB5
20	45	59.2	316	2	093J77
21	45	59.2	495	2	09VHX1
22	44	57.9	143	2	07QAC3
23	44	57.9	441	2	062GB2
24	44	57.9	441	2	0630S9
25	44	57.9	485	2	0804G3
26	44	57.9	777	2	08MPZ3
27	44	57.9	780	1	YVU5_CAEEL
28	44	57.9	1645	2	07QKG9
29	43.5	57.2	174	2	08UHP2
30	43.5	57.2	192	2	07D0T7
31	43.5	57.2	1624	2	07PT13

32	43	56.6	155	2	092P15
33	43	56.6	157	2	06CVY2
34	43	56.6	182	2	08J0A6
35	43	56.6	182	2	08U0C6
36	43	56.6	212	2	0949F9
37	43	56.6	214	2	06H3Y0
38	43	56.6	392	2	08RZP8
39	43	56.6	420	2	08U4C7
40	43	56.6	445	2	07VID8
41	43	56.6	497	2	06NR00
42	43	56.6	979	1	PTPN_BOVIN
43	43	56.6	1583	2	08J2S9
44	43	56.6	1689	2	07Q532
45	43	56.6	1724	2	093927

## ALIGNMENTS

RESULT 1

06NYU8 PRELIMINARY; PRT; 340 AA.

AC 06NYU8;

DT 05-JUL-2004 (TREMblrel. 27, Created)

DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)

DE Heterogeneous nuclear ribonucleoprotein A/B.

GN Name=hnRnpA;

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;

OC Cyprinidae; Danio.

OK NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Ditchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stadelton M., Soares M.B., Bonaldo M.F., Casanovi P., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loughran N.A., Peters G.J., Adams R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.

RA Strausberg R.

RL EMBL; BC066454; AA066454.1; -.

DR ZFIN; ZDB-GENE-030131-185; hnRnpA.

DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.

DR GO; GO:0019013; C:viral nucleocapsid; IEA.

DR InterPro; IPR000504; RNA\_rec\_mot.

DR Pfam; PF00076; RRM\_1; 2.

DR SMART; SM00360; RRM; 2.

DR PROSITE; PS50102; RRM; 2.

DR PROSITE; PS00030; RRM\_NP\_1; UNKNOWN\_1.

KW Nucleocapsid; Ribonucleoprotein.

SEQUENCE 340 AA; 37110 MW; 75C4F9F7C5B60913 CRC64;





RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,  
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpsstra P.,  
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,  
 RA Vassarotti A., Viari A., Wamburt R., Wedler E., Wedler H.,  
 RA Welternegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,  
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,  
 RA Yoshikawa H., Danchin A.;  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 RT *subtilis*.";  
 RU Nature 390:249-256(1997).  
 DR EMBL: Z99107; CAB12505.2; -.  
 DR PIR: D6793; D6793.  
 KW Complete proteome.  
 SQ SEQUENCE 145 AA; 15916 MW; 19252CB3E95BAB17 CRC64;

Query Match 64.5%; Score 49; DB 2; Length 145;  
 Best Local Similarity 77.8%; Pred. No. 4.5;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GFGGHPGF 10  
 DB 37 GMYGHPGY 45

RESULT 5  
 ID Q7XPR9 PRELIMINARY; PRT; 793 AA.  
 AC Q7XPR9;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)  
 DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DN OSUNBA065017.12 protein.  
 CN Name=OSUNBA065017.12;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12447439; DOI=10.1038/nature01183;  
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,  
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Yang K., Yu S., Tang Y.,  
 RA Meng Q., Zhang L., Lu Y., Wu Y., Zhang L.S., Yu Z., Fan D.,  
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,  
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,  
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,  
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,  
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,  
 RA Han L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,  
 RA Han B.;  
 RT "Sequence and analysis of rice chromosome 4.";  
 RL Nature 420:316-320(2002).  
 DR EMBL: AL606682; CAE03487.2; -.  
 DR HSSP: Q99405; IMPT.  
 DR Gramene: Q7XPR9; -.  
 DR GO: GO:0008233; F:peptidase activity; IEA.  
 DR GO: GO:0004289; F:subtilisin activity; IEA.  
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR003137; PA.  
 DR InterPro: IPR000209; Pept\_S8\_S53.  
 DR InterPro: IPR009020; Prot\_inh\_propept.  
 DR InterPro: IPR010259; Prot\_inh\_S8A.  
 DR Pfam: PF02225; PA; 1.  
 DR Pfam: PF00082; Peptidase\_S8; 1.  
 DR Pfam: PF05922; Subtilisin\_N; 1.  
 DR PRINTS: PR00723; SUBTILISIN.  
 DR PROSITE: PS00136; SUBTILASIN; UNKNOWN\_1.  
 DR PROSITE: PS00138; SUBTILASIN; 1.  
 SQ SEQUENCE 793 AA; 83568 MW; 920B578B2A4700C0 CRC64;

Query Match 63.2%; Score 48; DB 2; Length 793;  
 Best Local Similarity 63.6%; Pred. No. 38;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 BGFYGHGPF 11  
 DB 171 DGIYAGHPSFD 181

RESULT 6  
 ID Q8CIR3 PRELIMINARY; PRT; 117 AA.  
 AC Q8CIR3;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DN CARG-binding factor A (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22201804; PubMed=12086581;  
 RA Dean J.L., Sully G., Walt R., Rawlinson L., Clark A.R., Saklatvala J.;  
 RT "Identification of a novel AU-rich-element-binding protein which is  
 RT related to AUP1.";  
 RL Biochem J 366:709-719(2002).  
 DR EMBL: AY137376; AAAS3116.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 117 AA; 13081 MW; 0B90B9695732A60 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 117;  
 Best Local Similarity 63.6%; Pred. No. 11;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GFGGHPGFDY 12  
 DB 84 GYGYGPGYDY 94

RESULT 7  
 ID Y137\_ADE02 STANDARD; PRT; 137 AA.  
 AC P03293;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE Hypothetical protein B-137.  
 OS Human adenovirus type 2.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=10515;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83056843; PubMed=7142161;  
 RA Gingers T.R., Sciaky D., Gelinas R.E., Bing-Dong J., Yen C.E.,  
 RA Kelly M.M., Bullock P.A., Parsons B.L., O'Neill K.E., Roberts R.J.;  
 RT "Nucleotide sequences from the adenovirus-2 genome.";  
 RL J. Biol. Chem. 257:13475-13491(1982).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83056844; PubMed=7142162;  
 RA Alstrom P., Akusjervi G., Petersson M., Petersson U.;  
 RT "DNA sequence analysis of the region encoding the terminal protein and  
 RT the hypothetical N-gene product of adenovirus type 2.";  
 RL J. Biol. Chem. 257:13492-13498(1982).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

DR EMBL: J01917; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: E92351; A03865.  
 KM Hypothetical protein.  
 SQ SEQUENCE 137 AA; 14356 MW; B7ACA61A63116956 CRC64;

Query Match 60.5%; Score 46; DB 1; Length 137;  
 Best Local Similarity 54.5%; Pred. No. 13;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFGYGHGPF 11  
 Db 75 GFGYGHGPF 85

## RESULT 8

Q7VWMS PRELIMINARY; PRT; 196 AA.

AC Q7VWMS; 01-OCT-2003 (TEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Putative lipoprotein.  
 GN OrderedLocusNames=BP2072;  
 OS Bordetella pertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OX NCBI\_TaxID=520;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Tohama 1 / ATCC BAA-589 / NCTC 13251;  
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,  
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
 RA Achman M., Atkin R., Baker S., Basham D., Bacon N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Fellwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,  
 RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,  
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,  
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:32-40(2003).  
 KM EMBL: BX640417; CAE42350.1; -;  
 DR Complete proteome; Lipoprotein.  
 SQ SEQUENCE 196 AA; 21519 MW; FF6E2E86B5E9968 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 196;  
 Best Local Similarity 63.6%; Pred. No. 19;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GFGYGHGPF 12  
 Db 114 GFGYGHGPF 124

## RESULT 9

Q7W9K1 PRELIMINARY; PRT; 196 AA.

AC Q7W9K1; 01-OCT-2003 (TEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Putative lipoprotein.  
 GN OrderedLocusNames=BP1756;  
 OS Bordetella parapertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OX NCBI\_TaxID=519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=12822 / ATCC BAA-587;

RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,  
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
 RA Achman M., Atkin R., Baker S., Basham D., Bacon N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Fellwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,  
 RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,  
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,  
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:32-40(2003).  
 DR EMBL: BX640428; CAE37057.1; -;  
 KM Complete proteome; Lipoprotein.  
 SQ SEQUENCE 196 AA; 21562 MW; D082FBA6AC3A765 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 196;  
 Best Local Similarity 63.6%; Pred. No. 19;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GFGYGHGPF 12  
 Db 114 GFGYGHGPF 124

## RESULT 10

O80XR6 PRELIMINARY; PRT; 311 AA.

AC O80XR6; 01-JUN-2003 (TEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE Hnrpb protein.  
 GN Name=Hnrpb;  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Krausberg R.L., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC043069; AAH43069.1; -;  
 DR HSSP: Q14103; 1HD1.  
 DR MGI: MGI:1330294; Hnrpb.  
 DR InterPro: IPR000504; RNA\_rec\_mct.

DR Pfam; PF00076; RRM\_1; 2.  
 DR SMART; SM00360; RRM; 2.  
 DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
 SQ SEQUENCE 311 AA; 35816 MW; BC23A2644B9B3025 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 311;  
 Best Local Similarity 63.6%; Pred. No. 31;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYGGHPGPDY 12  
 DB 299 GYGGHPGPDY 309

## RESULT 11

ID Q7ZE9 PRELIMINARY; PRT; 324 AA.  
 AC Q7ZE9  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hnnpab-prov protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC NCBI\_TaxID=8355;

OX NCBI\_TaxID=8355;

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Ditchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalón D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Richardson S., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Maira M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Embryo;

RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.,

RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative.";

RT Dev. Dyn. 225:384-391 (2002).

RL [3]

RN SEQUENCE FROM N.A.

RP TISSUE=Embryo;

RC Klein S., Strausberg R.,

RA Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.

DR EMBL; BC043814; AA043814.1; -

DR HSSP; Q14103; 1HD1.

DR InterPro; IPR000504; RNA\_rec\_mot.

DR Pfam; PF00076; RRM\_1; 2.

DR SMART; SM00360; RRM; 2.

DR PROSITE; PS50102; RRM; 2.

DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.

SQ SEQUENCE 324 AA; 35785 MW; BBB8413ACD2F6456 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 324;  
 Best Local Similarity 63.6%; Pred. No. 32;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYGGHPGPDY 12  
 DB 291 GYGGHPGPDY 301

## RESULT 12

ID Q6GM69 PRELIMINARY; PRT; 326 AA.  
 AC Q6GM69;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC NCBI\_TaxID=8355;

OX NCBI\_TaxID=8355;

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Ditchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalón D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Richardson S., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Maira M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Kidney;

RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.,

RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative.";

RT Dev. Dyn. 225:384-391 (2002).

RL [3]

RN SEQUENCE FROM N.A.

RP TISSUE=Kidney;

RC Klein S., Strausberg R.,

RA Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.

DR EMBL; BC074212; AA074212.1; -

DR InterPro; IPR000504; RNA\_rec\_mot.

DR Pfam; PF00076; RRM\_1; 2.

DR SMART; SM00360; RRM; 2.

DR PROSITE; PS50102; RRM; 2.

DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.

KX Hypothetical protein.

SQ SEQUENCE 326 AA; 35938 MW; F6517A4610F31F2C CRC64;

Query Match 60.5%; Score 46; DB 2; Length 326;  
 Best Local Similarity 63.6%; Pred. No. 32;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



FT VARSPLIC 163 164 /FTid=VSP\_007827.  
 FT VARSPLIC 264 310 SP -> A (in isoform 2 and isoform 3).  
 FT VARSPLIC 264 310 /FTid=VSP\_007828.  
 FT VARSPLIC 264 310 Missing (in isoform 3 and isoform 4).  
 FT VARSPLIC 264 310 /FTid=VSP\_007829.  
 SQ SEQUENCE 331 AA; 36613 MW; B49C2PD9CF220ADC CRC64;

Query Match 60.5%; Score 46; DB 1; Length 331;  
 Best Local Similarity 63.6%; Pred. No. 33;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYGYGHPGPDY 12  
 DB 298 GYGYGHPGPDY 308

RESULT 14  
 088311 PRELIMINARY; PRT; 331 AA.

ID 088311  
 AC 088311  
 DT 01-NOV-1998 (TRENBLrel. 08, Created)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE ALP-C1.  
 GN Name=alp-c1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21142401; PubMed=11245986; DOI=10.1016/S0378-1119(00)00592-8;  
 RA Yabuki T., Miyagi S., Ueda H., Saitoh Y., Tsubumi K.;  
 RT "A novel growth-related nuclear protein binds and inhibits rat  
 aldolase B gene promoter."  
 RL Gene 264:123-129(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ito K.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB016536; BAA32032.1; -.  
 DR PIR; PC4375; PC4375.  
 DR PIR; PC4376; PC4376.  
 DR PIR; PC4377; PC4377.  
 DR HSP; Q14103; 1HD1.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00076; RRM\_1; 2.  
 DR SMART; SM00360; RRM; 2.  
 DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
 SQ SEQUENCE 331 AA; 36206 MW; 89F3B53FC595A54 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 331;  
 Best Local Similarity 63.6%; Pred. No. 33;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYGYGHPGPDY 12  
 DB 298 GYGYGHPGPDY 308

RESULT 15

090X81 PRELIMINARY; PRT; 332 AA.  
 AC 090X81  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Type A/B hnRNP p40 (Heterogeneous nuclear ribonucleoprotein).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Leverrier S., Cinato E., Paul C., Derancourt J., Bemark M.,  
 RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AJ238854; CAB62553.1; -.  
 DR PIR; PC4375; PC4375.  
 DR PIR; PC4376; PC4376.  
 DR PIR; PC4377; PC4377.  
 DR HSP; Q14103; 1HD1.  
 DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.  
 DR GO; GO:0019013; C:viral nucleocapsid; IEA.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00076; RRM\_1; 2.  
 DR SMART; SM00360; RRM; 2.  
 DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
 DR Nucleocapsid; Ribonucleoprotein.  
 SQ SEQUENCE 332 AA; 36233 MW; 414CE08E42A5F921 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 332;  
 Best Local Similarity 63.6%; Pred. No. 33;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYGYGHPGPDY 12  
 DB 299 GYGYGHPGPDY 309

Search completed: Match 1, 2005, 17:43:15  
 Job time : 79.7231 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 119.631 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-18

Perfect score: 75

Sequence: 1 KSSQSLSSRRKNYL 16

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneeqp1980s:\*  
2: geneeqp1990s:\*  
3: geneeqp2000s:\*  
4: geneeqp2001s:\*  
5: geneeqp2002s:\*  
6: geneeqp2003as:\*  
7: geneeqp2003bs:\*  
8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	17	3	AAV32226 G-CSF ago
2	72	96.0	17	2	AAV76082 MAB 55.1
3	72	96.0	218	7	ADD05274 Female mo
4	72	96.0	218	8	ADM80365 Murine ho
5	72	96.0	219	2	AAV76086 MAB 55.1
6	72	96.0	239	2	AAV76087 MAB 55.1
7	72	96.0	244	8	ADR59117 Anti-K88/
8	72	96.0	288	2	AAW82743 Fusion pr
9	72	96.0	673	2	AAW82742 Plasmid p
10	68	90.7	17	3	AAW82742 Plasmid p
11	68	90.7	110	6	AAW56520 Anti-DNA
12	68	90.7	111	6	AAW56520 Anti-DNA
13	68	90.7	111	6	ABR42303 Mouse mon
14	68	90.7	111	6	ABR42303 Mouse mon
15	68	90.7	113	7	ADC03128 Colon spe
16	68	90.7	115	8	ADC03128 Colon spe
17	68	90.7	132	3	AAW07964 Amino aci
18	68	90.7	132	3	AAW07964 Amino aci
19	68	90.7	219	2	AAW44495 Sequence
20	68	90.7	246	8	ADD27057 Human ant
21	68	90.7	247	7	ADC03132 Colon spe
22	68	90.7	249	2	AAW60770 Single ch
23	68	90.7	267	6	ABR42292 Bispicifi
24	68	90.7	267	6	ABR42292 Bispicifi
25	68	90.7	267	6	ABR42296 Bispicifi
			267	6	ABR42294 Bispicifi

26	68	90.7	268	6	ABR42288	AbR42288 Diabody 6
27	68	90.7	268	6	ABR42287	AbR42287 Diabody 6
28	68	90.7	268	6	ABR42286	AbR42286 Diabody 6
29	68	90.7	268	6	ABR42297	AbR42297 Diabody h
30	68	90.7	268	6	ABR83644	AbR83644 h679-scfv
31	68	90.7	268	6	ABR83643	AbR83643 679-scfv
32	68	90.7	391	6	ABR83649	AbR83649 TSI VL ch
33	65	86.7	117	2	AAW70908	CDR1 of t
34	65	86.7	100	2	AAW70948	light cha
35	65	86.7	265	2	AAW52864	Glycophor
36	64	85.3	208	7	ADD05282	Female mo
37	63	84.0	117	7	ADD94188	Mouse HUI
38	63	84.0	116	3	AAV15673	Murine 5B
39	60	80.0	113	2	AAV50145	Antibody
40	60	80.0	113	2	AAV50143	Antibody
41	60	80.0	113	2	AAV50144	Antibody
42	60	80.0	113	2	AAV21818	11E10 ant
43	60	80.0	113	6	ABR98748	Human res
44	60	80.0	113	6	ABR98749	Human res
45	60	80.0	113	6	ABR98747	Human res

## ALIGNMENTS

RESULT 1	AAV32226	standard; peptide; 17 AA.
ID	AAV32226	
XX	AAV32226;	
AC	15-FEB-2000	(first entry)
XX		
DT		
DE	G-CSF agonist antibody mab163-93 light chain variable region CDR1.	
XX		
XX	Granulocyte colony stimulating factor receptor; G-CSF; mouse;	
KW	monoclonal antibody; agonist; screening; neutropenia; therapy;	
KW	complementarity determining region; CDR; mab163-93.	
XX		
OS	Mus musculus.	
XX		
PN	WO955735-A1.	
XX		
PD	04-NOV-1999.	
XX		
PF	30-APR-1999;	99WO-US009466.
XX		
PR	30-APR-1998;	98US-0083575P.
XX		
PA	(TANO-) TANOX INC.	
XX		
PI	Ni B, Sun BNC, Sun CRY;	
XX		
DR	WPI, 2000-052805/04.	
XX		
PT	Treatment of neutropenia by stimulating proliferation of neutrophilic	
XX	cell lineage progenitors.	
PS	Claim 13; Page 30; 64pp; English.	
XX		
CC	The present sequence represents complementarity determining region 1	
CC	(CDR1) of the light chain variable region of murine monoclonal antibody	
CC	mab163-93. This antibody is an example of an agonist molecule that	
CC	specifically binds to or interacts with human granulocyte colony	
CC	stimulating factor (G-CSF) receptor to stimulate cell proliferation and	
CC	differentiation, especially by dimerising the receptor or activating	
CC	phosphorylation of kinases associated with the receptor. Agonist	
CC	antibodies can be used to stimulate proliferation of G-CSF-dependent	
CC	cells, e.g. to differentiate leading to a repopulation of neutrophilic	
CC	granulocyte lineage cells, especially to treat neutropenia (claimed).	
XX	They can also be used to detect human G-CSF receptor immunologically	
XX	Sequence 17 AA:	
SG		

Query Match 100.0%; Score 75; DB 3; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRTRKNYL 16  
 |||||  
 DB 1 KSSQSLSSRRTRKNYL 16

RESULT 2  
 AAR76082  
 ID AAR76082 standard; peptide; 17 AA.

XX AAR76082;  
 AC 25-MAR-2003 (revised)  
 DT 21-NOV-1995 (first entry)  
 XX  
 DE Mab 55.1 light chain CDR1.

XX Antigen binding structure; complementarity determining region; CDR;  
 KM CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
 KM monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;  
 KM transgenic animal; transgenic plant; antibody engineering;  
 KM humanized antibody; immunotoxin.

XX Mus sp.

PN W09515382-A1.

PD 08-JUN-1995.

PF 29-NOV-1994; 94MO-GB002610.

PR 03-DEC-1993; 93GB-00024819.

PR 03-JUN-1994; 94GB-00011089.

XX (ZENE ) ZENECA LTD.

PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
 PI Blakey DC;

DR WPI; 1995-215262/28.

XX Antigen binding structures containing CDR's recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
 PT and therapy of cancer.

PS Claim 2; Page 97; 121pp; English.

XX An antigen binding structure is based on the CDRE (given in AAR76078- 84)  
 CC of the heavy and light chains of Mab 55.1 (ECCAC 93081901), which  
 CC recognises the colorectal tumor-associated antigen CA55.1. It is  
 CC optionally humanized and in the form F(ab')<sub>2</sub>, F(ab)'<sub>2</sub>, Fab, Fv, scFv or V-  
 CC min, and is produced in transgenic animals or plants. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 17 AA;

Query Match 96.0%; Score 72; DB 2; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 8.6e-06;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRTRKNYL 16  
 |||||  
 DB 1 KSSQSLSSRRTRKNYL 16

RESULT 3  
 ADD05274  
 ID ADD05274 standard; protein; 218 AA.

AC ADD05274;

XX 01-JAN-2004 (first entry)

DT Female mouse sex hormone of the invention #6.

XX female sex hormone.

XX Mus sp.

PN W02003074704-A1.

PD 12-SEP-2003.

PF 28-FEB-2003; 2003MO-JP002311.

PR 01-MAR-2002; 2002JP-00055669.

PA (TAKE ) TAKEDA CHEM IND LTD.

PI Katagiri M, Fujimoto S, Goda Y;

DR WPI; 2003-731681/69.

DR N-PSDB; ADD05273.

XX Novel proteins for binding, identifying and concentrating female sex  
 PT hormones.

PS Claim 1; SEQ ID NO 12; 101pp; Japanese.

XX The present invention relates to proteins that bind to female sex  
 CC hormones. The method is useful for binding, identifying and concentrating  
 CC female sex hormones. The present invention represents a female sex  
 CC hormone of the invention.

XX Sequence 218 AA;

Query Match 96.0%; Score 72; DB 7; Length 218;  
 Best Local Similarity 93.8%; Pred. No. 0.00016;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRTRKNYL 16  
 |||||  
 DB 24 KSSQSLSSRRTRKNYL 39

RESULT 4  
 ADM80365  
 ID ADM80365 standard; protein; 218 AA.

XX ADM80365;

XX 03-JUN-2004 (first entry)

DT Murine hormone disruptor E2-3 antibody (scFv) protein SeqID 12.

XX antibody; mouse; murine; scFv; hormone disruptor; alkylphenol;

XX resin component; chlorophenol; immunological isolation;

XX environmental protection.

XX Mus sp.

PN W02003101611-A1.

PD 11-DEC-2003.

PF 30-MAY-2003; 2003MO-JP006840.

PR 31-MAY-2002; 2002JP-00159728.

PA (NIEN-) JAPAN ENVIROCHEMICALS LTD.  
 PA (ENVI-) ENVIRONMENT PURIFICATION RES INST INC.



PI Saito K, Shiraishi T, Goda Y;  
 XX MPI: 2004-043011/04.  
 DR N-PSDB; ADM80364.  
 XX  
 PT Polymer-molded support carrying anti-hormone-disrupting-substance  
 PT antibody for immunological isolation, concentration or clean-up of such  
 PT trace hormone disruptors in samples, applicable in environmental  
 PT protection.  
 XX  
 PS Example 7; SEQ ID NO 12; 133pp; Japanese.  
 XX  
 CC This invention relates to a novel material useful for the isolation of  
 CC hormone disrupting substances (i.e. hormone disruptors). Specifically, it  
 CC refers to a material that comprises a polymer-molded support carrying an  
 CC anti-hormone disruptor antibody covalently linked via a graft chain to  
 CC the support, which can be used to capture and subsequently recover the  
 CC substances of interest. The present invention provides a method for  
 CC selectively and efficiently concentrating hormone disruptors including  
 CC allylphenols, resin components, chlorophenols and female, male or thyroid  
 CC hormones from environmental samples. In particular, the method is useful  
 CC for the immunological isolation, concentration or clean-up of such trace  
 CC hormone disruptors that occur in river water, such that it is a method  
 CC applicable for environmental protection and the analytical sciences. This  
 CC polypeptide is a murine hormone disruptor antibody (scFv) protein  
 CC sequence of the invention.  
 CC  
 SQ Sequence 218 AA;  
 Query Match 96.0%; Score 72; DB 8; Length 218;  
 Best Local Similarity 93.8%; Pred. No. 0.00016;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KSSOSLSSRRKNTL 16  
 |||||:|||||  
 Db 24 KSSOSLNSRRKNTL 39  
 |||||:|||||  
 RESULT 5  
 AAR76086  
 ID AAR76086 standard; peptide; 219 AA.  
 XX  
 AC AAR76086;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-NOV-1995 (first entry)  
 XX  
 DE MAb 55.1 light chain.  
 XX  
 KW Antigen binding structure; complementarity determining region; CDR;  
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
 KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
 KW transgenic animal; transgenic plant; antibody engineering;  
 KW humanized antibody; immunotoxin.  
 XX  
 OS Mus sp.  
 XX  
 FN WO9515382-A1.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 29-NOV-1994; 94WO-GB002610.  
 XX  
 PR 03-DEC-1993; 93GB-00024819.  
 PR 03-JUN-1994; 94GB-00011089.  
 XX  
 PA (ZENEC) ZENECA LTD.  
 XX  
 PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
 PI Blakey DC;  
 XX  
 DR MPI, 1995-215262/28.  
 XX

PT Antigen binding structures containing CDR's recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
 PT and therapy of cancer.  
 XX  
 PS Claim 3; Page 98; 121pp; English.  
 XX  
 CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
 CC of the heavy (AAR76085) and light (AAR76086) chains of MAb 55.1 (ECCAC  
 CC 93081901), which recognises the colorectal tumor-associated antigen  
 CC CA55.1. It is optionally humanized and in the form F(ab)'<sub>2</sub>, Fab,  
 CC Fv, scFv or V-min, and is produced in transgenic animals or plants.  
 CC (Updated on 25-MAR-2003 to correct FN field.)  
 CC  
 SQ Sequence 219 AA;  
 Query Match 96.0%; Score 72; DB 2; Length 219;  
 Best Local Similarity 93.8%; Pred. No. 0.00016;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KSSOSLSSRRKNTL 16  
 |||||:|||||  
 Db 24 KSSOSLNSRRKNTL 39  
 |||||:|||||  
 RESULT 6  
 AAR76087  
 ID AAR76087 standard; protein; 239 AA.  
 XX  
 AC AAR76087;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-NOV-1995 (first entry)  
 XX  
 DE MAb 55.1 light chain  
 XX  
 KW Antigen binding structure; complementarity determining region; CDR;  
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
 KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
 KW transgenic animal; transgenic plant; antibody engineering;  
 KW humanized antibody; immunotoxin.  
 XX  
 OS Mus sp.  
 XX  
 FN WO9515382-A1.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 29-NOV-1994; 94WO-GB002610.  
 XX  
 PR 03-DEC-1993; 93GB-00024819.  
 PR 03-JUN-1994; 94GB-00011089.  
 XX  
 PA (ZENEC) ZENECA LTD.  
 XX  
 PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
 PI Blakey DC;  
 XX  
 DR MPI, 1995-215262/28.  
 DR N-PSDB; AAQ94036.  
 XX  
 PT Antigen binding structures containing CDR's recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
 PT and therapy of cancer.  
 XX  
 PS Disclosure; Fig 16; 121pp; English.  
 XX

CC MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated  
 CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)  
 CC chains of 55.1 were isolated, and F(ab)'<sub>2</sub>, Fab, scFv or V-min  
 CC humanized 55.1 constructs have been expressed in myeloma cells and E.  
 CC coli. (Updated on 25-MAR-2003 to correct FN field.)

XX SQ Sequence 239 AA;

Query Match 96.0%; Score 72; DB 2; Length 239;  
 Best Local Similarity 93.8%; Pred. No. 0.00018;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSRTRKNYL 16  
 DB 44 KSSQSLNSRTRKNYL 59

RESULT 7  
 ADR59117  
 ID ADR59117 standard; protein; 244 AA.

XX ADR59117;

XX DT 18-NOV-2004 (first entry)

XX DE Anti-K88/K99 antibody related protein, SEQ ID 68.

XX KW Gastrointestinal; antibody; heavy chain; light chain; variable region;  
 KW enterotoxigenic Escherichia coli; ETEC; K88 antigen; K99 antigen;  
 KW animal food; enteric disease.

XX OS Mus sp.

XX PN MO2004074491-A2.

XX PD 02-SEP-2004.

XX PF 16-FEB-2004; 2004MO-EP001427.

XX PR 18-FEB-2003; 2003US-0448429P.

XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX PI Brown D, Campos M, Dalmia B, Demarest S, Hansen G, Helfetz PB;

XX DR WPI; 2004-635583/61.

XX PT Novel immunoglobulin heavy chain comprising bovine CH3 or CH2 domain,  
 PT murine CH2CH3 domain of human CH2CH3 domain, useful in treatment or  
 PT prevention of enteric disease in animal.

XX PS Claim 58; SEQ ID NO 68; 165pp; English.

XX CC The present invention relates to coding sequences for mammalian antibody  
 CC heavy and light chains directed against enterotoxigenic Escherichia coli  
 CC (ETEC), in particular, ETEC of a strain possessing the K88 or K99  
 CC antigen. The heavy and light chain sequences are useful for producing  
 CC transgenic plants, which express the K88 or K99 antibody. The transgenic  
 CC plants are useful for producing animal feed, food product, animal feed  
 CC additive, feed pre-mix or nutritional supplement and are also useful for  
 CC treating or preventing enteric disease in an animal. The present sequence  
 CC was used in an example from the invention.

XX SQ Sequence 244 AA;

Query Match 96.0%; Score 72; DB 8; Length 244;  
 Best Local Similarity 93.8%; Pred. No. 0.00018;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSRTRKNYL 16  
 DB 43 KSSQSLNSRTRKNYL 58

RESULT 8  
 AAM82743  
 ID AAM82743 standard; protein; 288 AA.

XX AAM82743;

XX DT 10-MAY-1999 (first entry)

XX DE Fusion protein pNG4/55.1scFv/CPG2 R6/del EcorI.

XX KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;  
 KW prodrug-converting enzyme; cell surface antigen; treatment; cancer;  
 KW inflammation; rheumatoid arthritis; antibody; prodrug therapy system.

XX OS Synthetic.

XX PN WO9851787-A2.

XX PD 19-NOV-1998.

XX PF 05-MAY-1998; 98MO-GB001294.

XX PR 10-MAY-1997; 97GB-00009421.

XX PA (ZENEC ) ZENECA LTD.

XX PI Emery SC, Blakey DC;

XX DR WPI; 1999-059700/05.

XX DR N-PDB; AAV72064.

XX PT New gene construct expressing conjugate of targeting agent and prodrug-  
 PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
 PT drug in vivo, especially for treatment of cancer.

XX PS Example 15; Page 82; 100pp; English.

XX CC This sequence is a used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
 CC targeting group (I), and a heterologous prodrug-converting enzyme (II),  
 CC and (B) is directed to leave the cell for selective localisation at a  
 CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
 CC site, then administration of (II) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme prodrug therapy  
 CC system

XX SQ Sequence 288 AA;

Query Match 96.0%; Score 72; DB 2; Length 288;  
 Best Local Similarity 93.8%; Pred. No. 0.00022;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSRTRKNYL 16  
 DB 182 KSSQSLNSRTRKNYL 197

RESULT 9  
 AAM82742

ID AAM82742 standard; protein; 673 AA.

XX AAM82742;

XX DT 10-MAY-1999 (first entry)

XX DE Plasmid pNG4/55.1scFv/CPG2 R6 protein.

XX KW Conjugate; cell targeting; cytotoxic drug; prodrug-converting enzyme;  
 KW cell surface antigen; treatment; cancer; inflammation; antibody;

KW rheumatoid arthritis; prodrug therapy system.  
 XX Synthetic.  
 OS  
 XX WO9851787-A2.  
 XX  
 XX 19-NOV-1998.  
 XX  
 XX 05-MAY-1998; 98WO-GB001294.  
 XX  
 XX 10-MAY-1997; 97GB-00009421.  
 XX  
 XX (ZENEC) ZENEC LTD.  
 XX  
 XX Emery SC, Blakey DC;  
 XX  
 XX WPI; 1999-059700/05.  
 XX  
 XX N-PSDB; AAV72059.  
 XX  
 XX New gene construct expressing conjugate of targeting agent and prodrug-  
 PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
 PT drug in vivo, especially for treatment of cancer.  
 XX  
 XX Example 14; Page 78-79; 100pp; English.  
 XX  
 XX This sequence is used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
 CC targeting group (I) and a heterologous prodrug-converting enzyme (II),  
 CC and (B) is directed to leave the cell for selective localisation at a  
 CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
 CC site, then administration of (II) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme prodrug therapy  
 CC system  
 XX  
 XX Sequence 673 AA;  
 SQ  
 Query Match 96.0%; Score 72; DB 2; Length 673;  
 Best Local Similarity 93.8%; Pred. No. 0.00059;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KSSQSLSSRTKXNYL 16  
 Db 179 KSSQSLSSRTKXNYL 194  
 RESULT 10  
 AAB07951  
 ID AAB07951 standard; peptide; 17 AA.  
 XX  
 XX AAB07951;  
 XX  
 XX 14-NOV-2000 (first entry)  
 DE CDR1 sequence from an antibody with affinity for B7 molecules.  
 XX  
 XX Complementarity determining region; CDR; antibody; B7 molecule; B7-1;  
 KW B7-2; humanised immunoglobulin; autoimmune disease; infectious disease;  
 KW inflammatory disorder; systemic lupus erythematosus; diabetes mellitus;  
 KW insulin; asthma; arthritis; inflammatory bowel disease; cancer;  
 KW inflammatory dermatitis; multiple sclerosis; transplant rejection;  
 KW proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia;  
 KW thalassemia; aplastic anaemia; myeloid dysplasia syndrome.  
 XX  
 XX Mus sp.  
 XX  
 XX WO200047625-A2.  
 XX  
 XX 17-AUG-2000.  
 XX  
 XX 09-FEB-2000; 2000WO-US003303.

XX  
 PR 12-FEB-1999; 99US-00249011.  
 PR 24-JUN-1999; 99US-00339586.  
 XX  
 XX (GENY) GENETICS INST INC.  
 XX  
 XX Co MS, Vazquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 XX WPI; 2000-524532/47.  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases.  
 XX  
 XX Disclosure; Page 28; 162pp; English.  
 XX  
 XX The present sequence represents a complementarity determining region  
 CC (CDR) 1 from the light chains of an murine antibody with having a binding  
 CC specificity to B7-2 molecules. The sequence is used to construct  
 CC humanized immunoglobulins, which comprise an antigen binding region of  
 CC non-human origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulin, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient, and preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 90.7%; Score 68; DB 3; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 4.5e-05;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KSSQSLSSRTKXNYL 16  
 Db 1 KSSQSLSSRTKXNYL 16  
 RESULT 11  
 AAW56520  
 ID AAW56520 standard; protein; 110 AA.  
 XX  
 XX AAW56520;  
 XX  
 XX 28-SEP-1998 (first entry)  
 DE Anti-DNA IL/IM (H221) VL-JL sequence.  
 XX  
 XX Intracellular targeting sequence; DNA vaccine; genetic immunisation;  
 KW systemic lupus erythematosus; antibody; H221.  
 XX  
 XX Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Region 24..40  
 FT /label= CDR-I  
 FT 56..62  
 FT /label= CDR-II  
 FT 95..102  
 FT /label= CDR-III  
 XX  
 XX WO9817323-A1.  
 XX  
 XX 30-APR-1998.  
 XX  
 XX 23-OCT-1997; 97WO-US019545.

PR 23-OCT-1996; 96US-0029592P.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Williams WV, Madala M, Weiner DB;  
 XX  
 DR WPI; 1998-261198/23.  
 XX N-PSDB; AAV29839.  
 XX  
 PT Plasmid encoding immunogenic target protein - used in, e.g. protective or  
 PT therapeutic vaccines against allergy, cancer, microbial infection or auto  
 PT -immune disease.  
 XX  
 XX  
 PS Example 1; Page 31; 84pp; English.  
 XX  
 CC This polypeptide comprises the VL-JL sequence of anti-DNA IL/1M (H221)  
 CC antibody. This antibody binds to murine renal mesangial cells and aortic  
 CC endothelial cells, properties associated with pathogenic systemic lupus  
 CC erythematosus antibodies. H221 VH and VL DNA regions (see AAV29839-40)  
 CC have been amplified by PCR (see AAV29841-54) and used to generate VH and  
 CC Fv coding sequences. These were cloned into a genetic immunisation vector  
 CC and administered to mice for use in DNA vaccination studies. DNA  
 CC inoculation against the H221 VH and Fv regions elicited specific cellular  
 CC immune responses, particularly potent cytotoxic T lymphocyte (CTL)  
 CC responses, with enhancement in CTL activity by targeting the V region to  
 CC the cytosol or to the endoplasmic reticulum (ER). The invention provides  
 CC a novel plasmid comprising a sequence that encodes an immunogenic target  
 CC protein that includes, or is linked to, an intracellular targeting  
 CC sequence (see AAV5513-14) that directs localisation of the target  
 CC protein to the lysosome or ER. The novel plasmid is used as a protective  
 CC or therapeutic DNA vaccine to immunise against the immunogenic target  
 CC protein (claimed)  
 XX  
 SQ Sequence 110 AA;

Query Match 90.7%; Score 68; DB 2; Length 110;  
 Best Local Similarity 87.5%; Pred. No. 0.00039;  
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRTRKNYL 16  
 24 KSSQSLSSRRTRKNYL 39

RESULT 12  
 ABR42303  
 ID ABR42303 standard; protein; 111 AA.  
 XX  
 AC ABR42303;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Mouse monoclonal antibody 679 humanised light chain variable region.  
 XX  
 KW Diabody; antibody; humanised; histamine-succinyl-glycyl; HSG;  
 KM affinity enhancement system; tumour; targeting.  
 XX  
 OS Mus sp.  
 XX  
 FH Key  
 FT Region  
 FT Misc-difference 5  
 FT /label= FR1  
 FT Misc-difference 18  
 FT /note= "wild-type Ser substituted by Thr"  
 FT Misc-difference 18  
 FT /note= "wild-type Lys substituted by Arg"  
 FT Misc-difference 21  
 FT /note= "wild-type Met substituted by Leu"  
 FT Region 31..35  
 FT /label= CDR1  
 FT Region 36..49  
 FT /label= FR2  
 FT Region 50..66

FT /label= CDR2  
 FT Region 67..98  
 FT /label= FR3  
 FT Misc-difference 68  
 FT /note= "wild-type Thr substituted by Ser"  
 FT Region 99..108  
 FT /label= CDR3  
 FT Region 109..119  
 FT /label= FR3  
 XX  
 PN W02003033653-A2.  
 XX  
 XX  
 PD 24-APR-2003.  
 XX  
 PF 15-OCT-2002; 2002WO-US032717.  
 XX  
 PR 15-OCT-2001; 2001US-0328835P.  
 PR 21-DEC-2001; 2001US-0341881P.  
 XX  
 PA (IMMU-) IMMUNOMEDICS INC.  
 PA (IBCP-) IBC PHARM.  
 XX  
 PI Chang CK, Rossi E;  
 XX  
 DR WPI; 2003-393513/37.  
 XX

PT New kit comprising a multivalent, multi-specific binding protein and a  
 PT carrier molecule, useful for delivering a diagnostic/therapeutic agent  
 PT for treating cancer, and cardiovascular, immune, inflammatory, or  
 PT infectious diseases.  
 XX  
 XX  
 PS Disclosure; Fig 20; 87pp; English.

XX  
 CC The present sequence is the protein sequence of a humanised version of  
 CC the light chain variable region (VL) of murine monoclonal antibody 679  
 CC (see ABR42302). This antibody binds with high affinity to molecules  
 CC containing the moiety histamine-succinyl-glycyl (HSG). The present  
 CC humanised version of 679 VL has HSG binding affinity comparable to that  
 CC of the murine form. It was utilised in bispecific diabody constructs of  
 CC the invention (see ABR42297-99). These bispecific diabodies comprise an  
 CC HSG binding site and a carcinoembryonic antigen (CEA) binding site. They  
 CC are produced via recombinant DNA technology and create a novel affinity  
 CC enhancement system that shows specific affinity for HSG and CEA. The  
 CC diabodies pre-target CEA positive tumours for subsequent specific  
 CC delivery of therapeutic radioisotopes carried by HSG-carrying peptides.  
 CC Cancer, autoimmune diseases, infectious disease, cardiovascular diseases  
 CC and inflammatory diseases can be detected or treated using the methods of  
 CC the invention  
 XX  
 SQ Sequence 111 AA;

Query Match 90.7%; Score 68; DB 6; Length 111;  
 Best Local Similarity 87.5%; Pred. No. 0.00039;  
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRTRKNYL 16  
 24 KSSQSLSSRRTRKNYL 39

RESULT 13  
 ABR42302  
 ID ABR42302 standard; protein; 111 AA.  
 XX  
 AC ABR42302;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Mouse monoclonal antibody 679 light chain variable region.  
 XX  
 KW Diabody; antibody; histamine-succinyl-glycyl; HSG; mouse;  
 KM affinity enhancement system; tumour; targeting.  
 XX

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OS   Mus sp.
XX   Key
XX   Location/Qualifiers
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FT   1..23
FT   /label= FR1
FT   Region
FT   24..40
FT   /label= CDR1
FT   Region
FT   41..54
FT   /label= FR2
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FT   55..61
FT   /label= CDR2
FT   Region
FT   62..91
FT   /label= FR3
FT   Region
FT   92..100
FT   /label= CDR3
FT   Region
FT   101..111
FT   /label= FR3
XX   WO2003033653-A2.
XX   24-APR-2003.
XX   15-OCT-2002; 2002WO-US032717.
XX   15-OCT-2001; 2001US-0328835P.
XX   21-DEC-2001; 2001US-0341881P.
XX   (IMMU-) IMMUNOMEDICS INC.
XX   (IBCP-) IBC PHARM.
XX   Chang CK, Rossi E;
XX   WPI; 2003-393513/37.
XX   New kit comprising a multivalent, multi-specific binding protein and a
XX   carrier molecule, useful for delivering a diagnostic/therapeutic agent
XX   for treating cancer, and cardiovascular, immune, inflammatory, or
XX   infectious diseases.
XX   Disclosure; Fig 20; 87pp; English.
XX   The present sequence is the protein sequence of the light chain variable
XX   region (VL) of murine monoclonal antibody 679. This antibody binds with
XX   high affinity to molecules containing the moiety histamine-succinyl-
XX   glycy (HSG). A humanised version of 679 VL has been generated (see
XX   AB42303) that has HSG binding affinity comparable to that of the murine
XX   form. It was utilised in bispecific diabody constructs of the invention
XX   (see AB42297-99). These bispecific diabodies comprise an HSG binding
XX   site and a carcinoembryonic antigen (CEA) binding site. They are produced
XX   via recombinant DNA technology and create a novel affinity enhancement
XX   system that shows specific affinity for HSG and CEA. The diabodies pre-
XX   target CEA positive tumours for subsequent specific delivery of
XX   therapeutic radioisotopes carried by HSG-carrying peptides. Cancer,
XX   autoimmune diseases, infectious disease, cardiovascular diseases and
XX   inflammatory diseases can be detected or treated using the methods of the
XX   invention
XX   Sequence 111 AA;
SQ   Query Match 90.7%; Score 68; DB 6; Length 111;
      Best Local Similarity 87.5%; Pred. No. 0.00039;
      Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY   1 KSSQSLSSRRKRYL 16
      |||||:|||||
      24 KSSQSLFNSRRKRYL 39
      |||||:|||||
      ID   AD03128 standard; protein; 113 AA.
      AC   AD03128;

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```

XX   18-DEC-2003 (first entry)
XX   Colon specific antigen-p mucin murine antibody 679 Vκ protein.
XX   cytosolic; antitumour; antibody; colon specific antigen-p mucin;
XX   hapten binding site; immunconjugate; close-range lesion; tumour; ovary;
XX   thymus; parathyroid; spleen; carcinoma; gastrointestinal cancer;
XX   colorectal cancer; pancreatic cancer; ovarian cancer.
XX   Mus sp.
XX   Key
XX   Location/Qualifiers
FH   Domain
FT   24..40
FT   /note= "complementarity determining region 1"
FT   Domain
FT   56..62
FT   /note= "complementarity determining region 2"
FT   Domain
FT   95..102
FT   /note= "complementarity determining region 3"
XX   WO200282041-A2.
XX   17-OCT-2002.
XX   03-APR-2002; 2002WO-US010235.
XX   03-APR-2001; 2001US-00823746.
XX   (IMMU-) IMMUNOMEDICS INC.
XX   Hansen HJ, Griffiths GL, Leung S, McBride WJ, Qu Z;
XX   Goldenberg DM;
XX   WPI; 2003-167089/16.
XX   N-PSDB; AD031179.
XX   Novel multivalent, multispecific antibody for detecting/treating tumors
XX   expressing colon specific antigen-p mucin in mammal, comprises antigen
XX   and hapten binding sites.
XX   Disclosure; Fig 1; 202pp; English.
XX   The invention relates to a multivalent, multispecific antibody or its
XX   fragment comprising one more antigen binding sites having affinity
XX   towards colon specific antigen-p mucin (CSAP) target antigen and one or
XX   more hapten binding sites having affinity towards hapten molecules. The
XX   antibody is useful for screening a targetable conjugate. A therapeutic
XX   immunconjugate comprising the antibody is useful for detecting close-
XX   range lesion. The antibody or immunconjugate are also useful for
XX   delivering a diagnostic/detection or therapeutic agent, or their
XX   combination, to a target. The antibody or a targetable conjugate are
XX   useful for detecting or treating tumours expressing CSAP in a mammal, for
XX   imaging malignant tissue or normal tissue or cells in a mammal, for
XX   CSAP, where the normal tissue is from ovary, thymus, parathyroid or
XX   spleen, for intraoperatively identifying/disclosing the diseased tissues
XX   expressing CSAP in a subject, and for endoscopic identification of
XX   diseased tissues expressing CSAP. They are also useful for intravascular
XX   identification of diseased tissues expressing CSAP, for detecting lesions
XX   during an endoscopic, laparoscopic, intravascular catheter or surgical
XX   procedure, and for detecting and treating target cells, tissues or
XX   pathogens in a mammal. A method using the antibody is useful for
XX   diagnosing or detecting a malignancy in a subject, where the malignancy
XX   is carcinoma, gastrointestinal cancer, colorectal or pancreatic cancer or
XX   ovarian cancer, the subject is human or a domestic pet. This sequence
XX   represents one of the antibodies of the invention.
XX   Sequence 113 AA;
SQ   Query Match 90.7%; Score 68; DB 7; Length 113;
      Best Local Similarity 87.5%; Pred. No. 0.0004;

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Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KSSQSLSSRTKKNYL 16  
 |||||:|||||  
 Db 24 KSSQSLSSRTKKNYL 39

RESULT 15  
 ADO32150  
 ID ADO32150 standard; protein; 115 AA.  
 XX  
 AC ADO32150;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX

DE Mouse anti-CD3 antibody light chain homologous protein SEQ ID NO:66.

KW anti-CD3 antibody; epitope-binding fragment;  
 KM complementarity-determining region; CDR; immunocjugate; cytostatic;  
 XX antibody; myelodysplastic syndrome; acute myeloid leukaemia;  
 KM chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.  
 XX

OS Mus musculus.

PN WO2004043344-A2.

PD 27-MAY-2004.

PF 05-NOV-2003; 2003MO-US032737.

PR 07-NOV-2002; 2002US-0424332P.

PA (IMMU-) IMMUNOGEN INC.

PI Hoffee MG, Tavares D, Lutz RJ;

DR WPI; 2004-411619/38.

PT New antibodies that bind to CD33, useful for treating a disease  
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute  
 PT or chronic myeloid leukemia.

PS Example 3; SEQ ID NO 66; 124pp; English.

CC The present invention describes an isolated anti-CD33 antibody or its  
 CC epitope-binding fragment comprising: (a) at least one complementarity-  
 CC determining region (CDR); or (b) at least heavy chain variable region  
 CC comprising 3 CDRs, and at least one light chain variable region, where  
 CC the CDR has the ability to bind CD33. Also described: (1) an  
 CC immunocjugate comprising the antibody or its epitope-binding fragment  
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or  
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical  
 CC composition comprising the immunocjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment; immunocjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment  
 CC immunocjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33.

CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents a mouse anti-CD33 antibody light chain homologous  
 CC amino acid sequence, which is used in an example from the present  
 CC invention.  
 CC

SQ Sequence 115 AA;

Query Match 90.7%; Score 68; DB 8; Length 115;  
 Best Local Similarity 87.5%; Pred. No. 0.00041;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKKNYL 16  
 |||||:|||||  
 Db 24 KSSQSLSSRTKKNYL 39

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 Job time: 121.631 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 31.2615 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-18  
Perfect score: 75  
Sequence: 1 KSSQSLSSRTRKNYL 16

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	96.0	17	1	US-08-353-400-30
2	72	96.0	219	1	US-08-353-400-34
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4	72	96.0	288	3	US-09-423-439-38
5	72	96.0	673	3	US-09-423-439-32
6	68	90.7	17	4	US-09-627-896B-16
7	68	90.7	110	3	US-08-957-001B-5
8	68	90.7	110	3	US-08-957-001B-24
9	68	90.7	110	3	US-09-496-301-5
10	68	90.7	110	3	US-09-496-301-24
11	68	90.7	132	4	US-09-627-896B-4
12	68	90.7	132	4	US-09-627-896B-8
13	68	90.7	239	4	US-09-627-896B-22
14	65	86.7	265	2	US-08-403-853-16
15	63	84.0	109	2	US-08-308-494A-23
16	60	80.0	113	4	US-09-301-593-2
17	60	80.0	113	4	US-09-301-593-4
18	60	80.0	113	4	US-09-301-593-6
19	60	80.0	113	4	US-09-301-593-32
20	60	80.0	113	4	US-09-301-593-33
21	60	80.0	113	4	US-09-301-593-34
22	60	80.0	114	3	US-08-929-856-66
23	60	80.0	133	4	US-09-301-593-24
24	60	80.0	220	4	US-09-301-593-17
25	60	80.0	240	4	US-09-301-593-28
26	60	80.0	240	4	US-09-301-593-36
27	57	76.0	113	3	US-08-579-378A-5

28	57	76.0	113	3	US-08-579-378A-6	Sequence 6, Appli
29	57	76.0	113	5	PCT-US93-11612-5	Sequence 5, Appli
30	57	76.0	113	5	PCT-US93-11612-6	Sequence 6, Appli
31	57	76.0	133	3	US-08-579-378A-2	Sequence 2, Appli
32	57	76.0	133	3	US-08-579-378A-10	Sequence 10, Appli
33	57	76.0	133	5	PCT-US93-11612-2	Sequence 2, Appli
34	57	76.0	133	5	PCT-US93-11612-10	Sequence 10, Appli
35	56	74.7	117	1	US-08-467-420A-10	Sequence 10, Appli
36	56	74.7	117	1	US-08-470-110A-10	Sequence 10, Appli
37	56	74.7	117	1	US-08-667-769A-10	Sequence 10, Appli
38	56	74.7	117	2	US-08-940-371-10	Sequence 10, Appli
39	56	74.7	117	3	US-08-637-647-10	Sequence 10, Appli
40	56	74.7	117	4	US-09-563-222C-26	Sequence 26, Appli
41	56	74.7	117	5	PCT-US95-17082A-10	Sequence 10, Appli
42	56	74.7	105	1	US-08-467-420A-16	Sequence 16, Appli
43	56	74.7	105	1	US-08-470-110A-16	Sequence 16, Appli
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45	56	74.7	105	3	US-08-637-647-16	Sequence 16, Appli

## ALIGNMENTS

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; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-30

Query Match 96.0%; Score 72; DB 1; Length 17;
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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KSSQSLSSRTRKNYL 16
Db 1 KSSQSLSSRTRKNYL 16

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US-08-353-400-34
; Sequence 34, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-34

Query Match 96.0%; Score 72; DB 1; Length 219;  
Best Local Similarity 93.8%; Pred. No. 6.8e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSTRKNYL 16  
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DB 24 KSSQSLNSTRKNYL 39

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Sequence 37, Application US/08353400  
Patent No. 5665357  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-37

Query Match 96.0%; Score 72; DB 1; Length 239;  
Best Local Similarity 93.8%; Pred. No. 7.4e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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|||||:|||||  
DB 44 KSSQSLNSTRKNYL 59

RESULT 4  
US-09-423-439-38  
Sequence 38, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-423-439-38

Query Match 96.0%; Score 72; DB 3; Length 288;  
Best Local Similarity 93.8%; Pred. No. 9e-05;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 182 KSSQSLNSTRKNYL 197

RESULT 5  
US-09-423-439-32  
Sequence 32, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999



CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-423-439-32

Query Match 96.0%; Score 72; DB 3; Length 673;  
Best Local Similarity 93.8%; Pred. No. 0.00022;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16  
Db 179 KSSQSLNSRTKRYL 194

RESULT 6  
US-09-627-896B-16  
Sequence 16, Application US/09627896B  
GENERAL INFORMATION:  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
APPLICANT: CARENNO, BEATRIZ  
APPLICANT: CELINKER, ABBIE CHERYL  
APPLICANT: COLLINS, MARY  
APPLICANT: GOLDMAN, SAMUEL  
APPLICANT: GRAY, GARY S.  
APPLICANT: KNIGHT, ANDREA  
APPLICANT: O'HARA, DENISE  
APPLICANT: RUP, BONITA  
APPLICANT: VELDMAN, GEERTUUDA M.  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
FILE REFERENCE: 08702.0081-01000  
CURRENT APPLICATION NUMBER: US/09/627.896B  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 16  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CDR1 of humanized  
OTHER INFORMATION: murine anti-human B7-2 light chain  
US-09-627-896B-16

Query Match 90.7%; Score 68; DB 4; Length 17;  
Best Local Similarity 87.5%; Pred. No. 2.3e-05;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16  
Db 1 KSSQSLNSRTRENYL 16

RESULT 7  
US-08-957-001B-5  
Sequence 5, Application US/08957001B  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madato, Michael

APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/957.001B  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3439  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
US-08-957-001B-5

Query Match 90.7%; Score 68; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16  
Db 24 KSSQSLNSRTKRYL 39

RESULT 8  
US-08-957-001B-24  
Sequence 24, Application US/08957001B  
GENERAL INFORMATION:  
PATENT NO. 6228621  
APPLICANT: Williams, William V.  
APPLICANT: Madato, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/957.001B  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-957-001B-24

Query Match 90.7%; Score 68; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16  
DB 24 KSSQSLFNSRTKRYL 39

RESULT 9  
US-09-496-301-5  
Sequence 5, Application US/09496301  
Patent No. 6248565  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madai, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565r1s  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
MOLECULE TYPE: peptide

US-09-496-301-5

Query Match 90.7%; Score 68; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16  
DB 24 KSSQSLFNSRTKRYL 39

RESULT 10  
US-09-496-301-24  
Sequence 24, Application US/09496301  
Patent No. 6248565  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madai, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565r1s  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-496-301-24

Query Match 90.7%; Score 68; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 0.00016;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16  
DB 24 KSSQSLFNSRTKRYL 39

RESULT 11  
US-09-627-896B-4  
Sequence 4, Application US/09627896B  
Patent No. 6827934  
GENERAL INFORMATION:  
APPLICANT: CO, MAN SUNG

```

: APPLICANT: VASQUEZ, MAXIMILIANO
: APPLICANT: CARENNO, BEATRIZ
: APPLICANT: CELNIKER, ABBIE CHERYL
: APPLICANT: COLLINS, MARY
: APPLICANT: GOLDMAN, SAMUEL
: APPLICANT: GRAY, GARY S.
: APPLICANT: KNIGHT, ANDREA
: APPLICANT: O'HARA, DENISE
: APPLICANT: RUP, BONITA
: APPLICANT: VELDMAN, GEERTRUUDA M.
: TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
: FILE REFERENCE: 08702.0081-01000
: CURRENT APPLICATION NUMBER: US/09/627,896B
: CURRENT FILING DATE: 2000-07-27
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 132
: TYPE: PRT
: ORGANISM: Murine sp.
: FEATURE:
: OTHER INFORMATION: Anti-B7-2 light chain
US-09-627-896B-4

Query Match          90.7%; Score 68; DB 4; Length 132;
Best Local Similarity 87.5%; Pred. No. 0.0002;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16
   |||||:||||:|
Db 44 KSSQSLSSRTKRYL 59

RESULT 12
US-09-627-896B-8
: Sequence 8, Application US/09627896B
: Patent No. 6827934
: GENERAL INFORMATION:
: APPLICANT: CO, MAN SUNG
: APPLICANT: VASQUEZ, MAXIMILIANO
: APPLICANT: CARENNO, BEATRIZ
: APPLICANT: CELNIKER, ABBIE CHERYL
: APPLICANT: COLLINS, MARY
: APPLICANT: GOLDMAN, SAMUEL
: APPLICANT: GRAY, GARY S.
: APPLICANT: KNIGHT, ANDREA
: APPLICANT: O'HARA, DENISE
: APPLICANT: RUP, BONITA
: APPLICANT: VELDMAN, GEERTRUUDA M.
: TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
: FILE REFERENCE: 08702.0081-01000
: CURRENT APPLICATION NUMBER: US/09/627,896B
: CURRENT FILING DATE: 2000-07-27
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 8
: LENGTH: 132
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Humanized
: OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-627-896B-8

Query Match          90.7%; Score 68; DB 4; Length 132;
Best Local Similarity 87.5%; Pred. No. 0.0002;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16
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Db 44 KSSQSLSSRTKRYL 59
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RESULT 13
US-09-627-896B-22
: Sequence 22, Application US/09627896B
: Patent No. 6827934
: GENERAL INFORMATION:
: APPLICANT: CO, MAN SUNG
: APPLICANT: VASQUEZ, MAXIMILIANO
: APPLICANT: CARENNO, BEATRIZ
: APPLICANT: CELNIKER, ABBIE CHERYL
: APPLICANT: COLLINS, MARY
: APPLICANT: GOLDMAN, SAMUEL
: APPLICANT: GRAY, GARY S.
: APPLICANT: KNIGHT, ANDREA
: APPLICANT: O'HARA, DENISE
: APPLICANT: RUP, BONITA
: APPLICANT: VELDMAN, GEERTRUUDA M.
: TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
: FILE REFERENCE: 08702.0081-01000
: CURRENT APPLICATION NUMBER: US/09/627,896B
: CURRENT FILING DATE: 2000-07-27
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 22
: LENGTH: 239
: TYPE: PRT
: ORGANISM: Mus sp.
: FEATURE:
: OTHER INFORMATION: 3D1 light chain
US-09-627-896B-22

Query Match          90.7%; Score 68; DB 4; Length 239;
Best Local Similarity 87.5%; Pred. No. 0.00037;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16
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Db 44 KSSQSLSSRTKRYL 59
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```

RESULT 14
US-08-403-853-16
: Sequence 16, Application US/08403853
: Patent No. 5844094
: GENERAL INFORMATION:
: APPLICANT: HUDSON, Peter J.
: APPLICANT: LAH, Maria
: APPLICANT: KORRT, Alex A.
: APPLICANT: IRVING, Robert A.
: APPLICANT: ATWELL, John L.
: APPLICANT: MALBY, Robyn L.
: APPLICANT: POWER, Barbara E.
: APPLICANT: COLMAN, Peter M.
: TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESS: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/403,853
: FILING DATE: 30-MAY-1995
: CLASSIFICATION: 435
```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU93/00491  
FILING DATE: 24-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL 4973  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-403-853-16

Query Match 86.7%; Score 65; DB 2; Length 265;  
Best Local Similarity 81.2%; Pred. No. 0.0014;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKKNYL 16  
DB 165 RSSQSLSSRTKKNYL 180

RESULT 15  
US-08-308-494A-23  
Sequence 23, Application US/08308494A  
Patent No. 5959083  
GENERAL INFORMATION:  
APPLICANT: Bogslet, Klaus  
APPLICANT: Seeman, Gerhard  
TITLE OF INVENTION: Tetravalent Bispecific Receptors, The  
TITLE OF INVENTION: Preparation and Use Thereof  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,494A  
FILING DATE: 21-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/891,739  
FILING DATE: 01-JUN-1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4118120.4  
FILING DATE: 03-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kulik, David J.  
REGISTRATION NUMBER: 36,576  
REFERENCE/DOCKET NUMBER: 05552-1186-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-308-494A-23

Query Match 84.0%; Score 63; DB 2; Length 109;  
Best Local Similarity 87.5%; Pred. No. 0.0012;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKKNYL 16  
DB 21 KSSQSLSSRTKKNYL 36

Search completed: March 1, 2005, 17:46:57  
Job time: 32.2615 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 85.6615 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-18  
Perfect score: 75  
Sequence: 1 KSSQSLSSRRKXNYL 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	75	100.0	16	14 US-10-071-962-18	Sequence 18, Appl
2	68	90.7	17	9 US-09-249-011A-16	Sequence 16, Appl
3	68	90.7	113	14 US-10-270-071-7	Sequence 7, Appl
4	68	90.7	113	14 US-10-270-071-8	Sequence 8, Appl
5	68	90.7	132	9 US-09-249-011A-4	Sequence 4, Appl
6	68	90.7	132	9 US-09-249-011A-6	Sequence 8, Appl
7	68	90.7	239	9 US-09-249-011A-22	Sequence 22, Appl
8	68	90.7	267	14 US-10-270-071-22	Sequence 22, Appl
9	68	90.7	267	14 US-10-270-071-26	Sequence 26, Appl
10	68	90.7	267	14 US-10-270-071-30	Sequence 30, Appl
11	68	90.7	267	14 US-10-270-071-36	Sequence 36, Appl
12	68	90.7	268	14 US-10-270-071-10	Sequence 10, Appl
13	68	90.7	268	14 US-10-270-071-12	Sequence 12, Appl

14	68	90.7	268	14	US-10-270-071-14	Sequence 14, Appl
15	68	90.7	268	14	US-10-270-071-16	Sequence 16, Appl
16	68	90.7	268	14	US-10-270-071-32	Sequence 32, Appl
17	68	90.7	268	14	US-10-328-190-2	Sequence 2, Appl
18	68	90.7	268	14	US-10-328-190-4	Sequence 4, Appl
19	68	90.7	358	16	US-10-829-388-12	Sequence 12, Appl
20	68	90.7	363	16	US-10-829-388-2	Sequence 2, Appl
21	68	90.7	391	14	US-10-328-190-14	Sequence 14, Appl
22	63	84.0	17	10	US-09-995-529-73	Sequence 73, Appl
23	63	84.0	17	11	US-09-995-529-73	Sequence 73, Appl
24	60	80.0	113	9	US-09-301-593-2	Sequence 2, Appl
25	60	80.0	113	9	US-09-301-593-4	Sequence 4, Appl
26	60	80.0	113	9	US-09-301-593-6	Sequence 6, Appl
27	60	80.0	113	9	US-09-301-593-32	Sequence 32, Appl
28	60	80.0	113	9	US-09-301-593-33	Sequence 33, Appl
29	60	80.0	113	9	US-09-301-593-34	Sequence 34, Appl
30	60	80.0	113	10	US-09-215-163-42	Sequence 42, Appl
31	60	80.0	113	14	US-10-121-464-2	Sequence 2, Appl
32	60	80.0	113	14	US-10-121-464-4	Sequence 4, Appl
33	60	80.0	113	14	US-10-121-464-6	Sequence 6, Appl
34	60	80.0	113	14	US-10-159-006-2	Sequence 2, Appl
35	60	80.0	113	14	US-10-159-006-4	Sequence 4, Appl
36	60	80.0	113	14	US-10-159-006-6	Sequence 6, Appl
37	60	80.0	113	14	US-10-159-006-32	Sequence 32, Appl
38	60	80.0	113	14	US-10-159-006-33	Sequence 33, Appl
39	60	80.0	113	14	US-10-159-006-34	Sequence 34, Appl
40	60	80.0	133	9	US-09-301-593-24	Sequence 24, Appl
41	60	80.0	133	14	US-10-159-006-24	Sequence 24, Appl
42	60	80.0	220	9	US-09-301-593-17	Sequence 17, Appl
43	60	80.0	220	14	US-10-159-006-17	Sequence 17, Appl
44	60	80.0	240	9	US-09-301-593-28	Sequence 28, Appl
45	60	80.0	240	9	US-09-301-593-36	Sequence 36, Appl

## ALIGNMENTS

## RESULT 1

US-10-071-962-18

Sequence 18, Application US/10071962

Publication No. US20030170237A1

GENERAL INFORMATION:

APPLICANT: Baifu Ni

APPLICANT: Bill N.C. Sun

TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and

FILE REFERENCE: 98-3 Screening Method Therefor

CURRENT FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US/09/303,155A

PRIOR FILING DATE: 1999-04-30

PRIOR APPLICATION NUMBER: 60/083,575

NUMBER OF SEQ ID NOS: 127

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 16

TYPE: PRT

ORGANISM: mouse

US-10-071-962-18

Query Match

Best Local Similarity

Matches 16; Conservative

1 KSSQSLSSRRKXNYL 16

1 KSSQSLSSRRKXNYL 16

1 KSSQSLSSRRKXNYL 16

1 KSSQSLSSRRKXNYL 16

1 KSSQSLSSRRKXNYL 16

1 KSSQSLSSRRKXNYL 16

1 KSSQSLSSRRKXNYL 16

1 KSSQSLSSRRKXNYL 16

```
/ Sequence 16, Application US/09249011A
/ Patent No. US20020176855A1
/ GENERAL INFORMATION:
/ APPLICANT: CO, MAN SUNG
/ APPLICANT: VASQUEZ, MAXIMILIANO
/ APPLICANT: CARENO, BEATRIZ
/ APPLICANT: CELINIKER, ABIE CHERYL
/ APPLICANT: COLLINS, MARY
/ APPLICANT: GOLDMAN, SAMUEL
/ APPLICANT: GRAY, GARY S.
/ APPLICANT: KNIGHT, ANDREA
/ APPLICANT: O'HARA, DENISE
/ APPLICANT: RUP, BONITA
/ APPLICANT: VELDMAN, GEERTRUIDA M.
/ TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
/ TITLE OF INVENTION: OF TREATMENT THEREWITH
/ FILE REFERENCE: 08702.0081-00000
/ CURRENT APPLICATION NUMBER: US/09/249,011A
/ CURRENT FILING DATE: 1999-02-12
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: CDRI of humanized
US-09-249-011A-16
```

```
Query Match          90.7%; Score 68; DB 9; Length 17;
Best Local Similarity 87.5%; Pred. No. 0.0001;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KSSQSLSSRTKRYL 16
DB 1 KSSQSLSSRTKRYL 16
```

```
RESULT 3
US-10-270-071-7
/ Sequence 7, Application US/10270071
/ Patent No. US2003013333A1
/ GENERAL INFORMATION:
/ APPLICANT: ROSSI, EDMUND
/ APPLICANT: CHANG, CHIEN-HSING KEN
/ TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
/ FILE REFERENCE: 042418/0110
/ CURRENT APPLICATION NUMBER: US/10/270,071
/ CURRENT FILING DATE: 2003-01-21
/ PRIOR APPLICATION NUMBER: 60/328,835
/ PRIOR FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 60/341,881
/ PRIOR FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 113
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
/ OTHER INFORMATION: sequence of m679VK
US-10-270-071-7
```

```
Query Match          90.7%; Score 68; DB 14; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.00074;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KSSQSLSSRTKRYL 16
DB 24 KSSQSLSSRTKRYL 39
```

```
RESULT 4
US-10-270-071-8
/ Sequence 8, Application US/10270071
/ Patent No. US2003013333A1
/ GENERAL INFORMATION:
/ APPLICANT: ROSSI, EDMUND
/ APPLICANT: CHANG, CHIEN-HSING KEN
/ TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
/ FILE REFERENCE: 042418/0110
/ CURRENT APPLICATION NUMBER: US/10/270,071
/ CURRENT FILING DATE: 2003-01-21
/ PRIOR APPLICATION NUMBER: 60/328,835
/ PRIOR FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 60/341,881
/ PRIOR FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 113
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-270-071-8
```

```
Query Match          90.7%; Score 68; DB 14; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.00074;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KSSQSLSSRTKRYL 16
DB 24 KSSQSLSSRTKRYL 39
```

```
RESULT 5
US-09-249-011A-4
/ Sequence 4, Application US/09249011A
/ Patent No. US20020176855A1
/ GENERAL INFORMATION:
/ APPLICANT: CO, MAN SUNG
/ APPLICANT: VASQUEZ, MAXIMILIANO
/ APPLICANT: CARENO, BEATRIZ
/ APPLICANT: CELINIKER, ABIE CHERYL
/ APPLICANT: COLLINS, MARY
/ APPLICANT: GOLDMAN, SAMUEL
/ APPLICANT: GRAY, GARY S.
/ APPLICANT: KNIGHT, ANDREA
/ APPLICANT: O'HARA, DENISE
/ APPLICANT: RUP, BONITA
/ APPLICANT: VELDMAN, GEERTRUIDA M.
/ TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
/ TITLE OF INVENTION: OF TREATMENT THEREWITH
/ FILE REFERENCE: 08702.0081-00000
/ CURRENT APPLICATION NUMBER: US/09/249,011A
/ CURRENT FILING DATE: 1999-02-12
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 132
/ TYPE: PRT
/ ORGANISM: Murine sp.
/ FEATURE:
/ OTHER INFORMATION: Anti-B7-2 light chain
US-09-249-011A-4
```

```
Query Match          90.7%; Score 68; DB 9; Length 132;
Best Local Similarity 87.5%; Pred. No. 0.00088;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KSSQSLSSRTKRYL 16
DB 1 KSSQSLSSRTKRYL 16
```

Db 44 KSSQSLNSRTRENYL 59

## RESULT 6

US-09-249-011A-8  
; Sequence 8, Application US/09249011A  
; Patent No. US20020176855A1  
; GENERAL INFORMATION:  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; APPLICANT: CARRENO, BEATRIZ  
; APPLICANT: CELINIKER, ABBIE CHERYL  
; APPLICANT: COLLINS, MARY  
; APPLICANT: GOLDMAN, SAMUEL  
; APPLICANT: GRAY, GARY S.  
; APPLICANT: KNIGHT, ANDREA  
; APPLICANT: O'HARA, DENISE  
; APPLICANT: RUP, BONITA  
; APPLICANT: VELDMAN, GEBERTUIDA M.  
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
; FILE REFERENCE: 08702.0081-00000  
; CURRENT APPLICATION NUMBER: US/09/249,011A  
; CURRENT FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanized  
; OTHER INFORMATION: murine anti-human B7-2 light chain  
US-09-249-011A-8

Query Match 90.7%; Score 68; DB 9; Length 132;  
Best Local Similarity 87.5%; Pred. No. 0.00088;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTKRYL 16  
Db 44 KSSQSLNSRTRENYL 59

## RESULT 7

US-09-249-011A-22  
; Sequence 22, Application US/09249011A  
; Patent No. US20020176855A1  
; GENERAL INFORMATION:  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; APPLICANT: CARRENO, BEATRIZ  
; APPLICANT: CELINIKER, ABBIE CHERYL  
; APPLICANT: COLLINS, MARY  
; APPLICANT: GOLDMAN, SAMUEL  
; APPLICANT: GRAY, GARY S.  
; APPLICANT: KNIGHT, ANDREA  
; APPLICANT: O'HARA, DENISE  
; APPLICANT: RUP, BONITA  
; APPLICANT: VELDMAN, GEBERTUIDA M.  
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
; FILE REFERENCE: 08702.0081-00000  
; CURRENT APPLICATION NUMBER: US/09/249,011A  
; CURRENT FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-249-011A-22

Query Match 90.7%; Score 68; DB 9; Length 239;  
Best Local Similarity 87.5%; Pred. No. 0.0016;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTKRYL 16  
Db 44 KSSQSLNSRTRENYL 59

## RESULT 8

US-10-270-071-22  
; Sequence 22, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIH-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: sequence of polypeptide 2 of BSI  
US-10-270-071-22

Query Match 90.7%; Score 68; DB 14; Length 267;  
Best Local Similarity 87.5%; Pred. No. 0.0018;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTKRYL 16  
Db 170 KSSQSLFNSRTKRYL 185

## RESULT 9

US-10-270-071-26  
; Sequence 26, Application US/10270071  
; Publication No. US20030113333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIH-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: sequence of polypeptide 2 of BSI.5  
US-10-270-071-26

Query Match 90.7%; Score 68; DB 14; Length 267;  
Best Local Similarity 87.5%; Pred. No. 0.0018;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRTKRYL 16  
|||||:|||||  
Db 170 KSSQSLFNSRTKRYL 185

RESULT 10  
US-10-270-071-30  
; Sequence 30, Application US/10270071  
; Publication No. US2003011333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/10/270,071  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-270-071-30

Query Match 90.7%; Score 68; DB 14; Length 267;  
Best Local Similarity 87.5%; Pred. No. 0.0018;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KSSQSLSSRTKRYL 16  
|||||:|||||  
Db 170 KSSQSLFNSRTKRYL 185

RESULT 11  
US-10-270-071-36  
; Sequence 36, Application US/10270071  
; Publication No. US2003011333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/10/270,071  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: sequence for polypeptide 1 of BSI.5H (h679XhM14 bispecific  
US-10-270-071-36

Query Match 90.7%; Score 68; DB 14; Length 267;  
Best Local Similarity 87.5%; Pred. No. 0.0018;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KSSQSLSSRTKRYL 16

Db 170 KSSQSLFNSRTKRYL 185  
|||||:|||||

RESULT 12  
US-10-270-071-10  
; Sequence 10, Application US/10270071  
; Publication No. US2003011333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/10/270,071  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-270-071-10

Query Match 90.7%; Score 68; DB 14; Length 268;  
Best Local Similarity 87.5%; Pred. No. 0.0019;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KSSQSLSSRTKRYL 16  
|||||:|||||  
Db 171 KSSQSLFNSRTKRYL 186

RESULT 13  
US-10-270-071-12  
; Sequence 12, Application US/10270071  
; Publication No. US2003011333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/10/270,071  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-270-071-12

Query Match 90.7%; Score 68; DB 14; Length 268;  
Best Local Similarity 87.5%; Pred. No. 0.0019;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KSSQSLSSRTKRYL 16  
|||||:|||||  
Db 171 KSSQSLFNSRTKRYL 186



## RESULT 14

US-10-270-071-14  
; Sequence 14, Application US/10270071  
; Publication No. US2003011333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-270-071-14

## Query Match

Best Local Similarity 90.7%; Score 68; DB 14; Length 268;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSOSLSSRTKNTL 16  
|||:|||||

Db 171 KSSOSLFNSRTKNTL 186

## RESULT 15

US-10-270-071-16  
; Sequence 16, Application US/10270071  
; Publication No. US2003011333A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSSI, EDMUND  
; APPLICANT: CHANG, CHIEN-HSING KEN  
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS  
; FILE REFERENCE: 042418/0110  
; CURRENT APPLICATION NUMBER: US/10/270,071  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/328,835  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/341,881  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-270-071-16

## Query Match

Best Local Similarity 90.7%; Score 68; DB 14; Length 268;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSSOSLSSRTKNTL 16  
|||:|||||

Db 171 KSSOSLFNSRTKNTL 186

Search completed: March 1, 2005, 17:52:51  
Job time : 86.6615 secs

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GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 21.6615 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-18

Perfect score: 75

Sequence: 1 KSSQSLSSRRKKNYL 16

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r79:\*  
2: p1r12:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	96.0	81	2	PH1048
2	72	96.0	101	2	PH1046
3	72	96.0	103	2	PH1047
4	72	96.0	112	2	S43103
5	72	96.0	113	2	PT0408
6	72	96.0	113	2	PT0407
7	72	96.0	120	2	G33932
8	71	94.7	104	2	PH1050
9	71	94.7	104	2	PH1101
10	71	94.7	104	2	PH1102
11	71	94.7	104	2	PH1103
12	71	94.7	104	2	PH1104
13	68	90.7	112	2	PH10265
14	67	89.3	103	2	PH1051
15	67	89.3	103	2	PH1052
16	66	88.0	111	2	S03304
17	64	85.3	97	2	A42575
18	63	84.0	94	2	S20648
19	63	84.0	113	2	PL0264
20	63	84.0	214	2	S68212
21	60	80.0	133	2	PS0023
22	59	78.7	113	2	PT0409
23	57	76.0	104	2	PH1053
24	57	76.0	113	2	JC2270
25	57	76.0	133	2	S38807
26	56	74.7	105	2	C30535
27	56	74.7	107	2	F30535
28	56	74.7	107	2	D30535
29	56	74.7	107	2	G30535

30	56	74.7	108	2	E30535	Ig kappa chain V r
31	56	74.7	112	2	F30538	Ig kappa chain V r
32	56	74.7	112	2	E30538	Ig kappa chain V r
33	56	74.7	113	2	PH0263	Ig kappa chain V r
34	56	74.7	113	2	S46373	Ig kappa chain V-J
35	55	73.3	112	2	S09970	Ig kappa chain V-J
36	55	73.3	112	2	S26040	Ig kappa chain pre
37	54	72.0	112	2	S41393	Ig kappa chain V r
38	54	72.0	118	2	PH0356	Ig kappa chain V r
39	53	70.7	113	2	A49260	antitumor monoclon
40	53	70.7	134	2	PC1214	Ig kappa chain pre
41	52	69.3	109	2	S26336	Ig light chain V r
42	51	68.0	101	2	S26337	Ig light chain V r
43	51	68.0	103	2	PH1054	Ig light chain V r
44	51	68.0	111	2	G30502	Ig kappa chain V r
45	50	66.7	92	2	S37532	Ig kappa chain V r

#### ALIGNMENTS

##### RESULT 1

PH1048

Ig light chain V region (clone 165.49) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996

C:Accession: PH1048

R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1048

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-81 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 96.0%; Score 72; DB 2; Length 81;  
Best Local Similarity 93.8%; Pred. No. 5.9e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRRKKNYL 16  
Db 3 KSSQSLSSRRKKNYL 18

##### RESULT 2

PH1046

Ig light chain V region (clone 202.9) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1046

R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1046

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-101 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 101;  
Best Local Similarity 93.8%; Pred. No. 7.4e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRRKKNYL 16  
Db 3 KSSQSLSSRRKKNYL 18

Db 24 KSSQSLNSRTRKNYL 39

RESULT 3

PH1047  
Ig light chain V region (clones 165.45 and 163-cl) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C/Accession: PH1047; PH1049  
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B  
A/Reference number: PH0971; PMID:92381444; PMID:1512540  
A/Accession: PH1047  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-103 <RTL>  
A/Experimental source: B cell, strain [NZB x NZW]F1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 103;  
Best Local Similarity 93.8%; Pred. No. 7.6e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSRTRKNYL 16  
|||||:|||||  
Db 24 KSSQSLNSRTRKNYL 39

RESULT 4

S43103  
Ig kappa chain V-J region (4B1 VL) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 24-May-2001  
C/Accession: S43103  
R/Gilbert, D.; Brard, F.; Margartite, C.; Delpech, A.; Tron, F.  
submitted to the EMBL Data Library, March 1994  
A/Description: An idiotype D23-bearing polypeptide, murine anti-DNA monoclonal antibody  
A/Reference number: S42484  
A/Accession: S43103  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-112 <GLU>  
A/Cross-references: NID:231353; NID:9467574; PIDN:CAA83231.1; PID:9467575  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 112;  
Best Local Similarity 93.8%; Pred. No. 8.2e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSRTRKNYL 16  
|||||:|||||  
Db 24 KSSQSLNSRTRKNYL 39

RESULT 5

PT0408  
Ig light chain V region (S107/VH11 group 1-6) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C/Accession: PT0408  
R/Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.  
J. Exp. Med. 173, 731-741, 1991  
A/Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi  
A/Reference number: PT0376; PMID:9147903; PMID:1900082  
A/Accession: PT0408  
A/Molecule type: DNA  
A/Residues: 1-113 <BEH>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin  
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 113;  
Best Local Similarity 93.8%; Pred. No. 8.3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSRTRKNYL 16  
|||||:|||||  
Db 24 KSSQSLNSRTRKNYL 39

RESULT 6

PT0407  
Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C/Accession: PT0407  
R/Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.  
J. Exp. Med. 173, 731-741, 1991  
A/Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi  
A/Reference number: PT0376; PMID:9147903; PMID:1900082  
A/Accession: PT0407  
A/Molecule type: DNA  
A/Residues: 1-113 <BEH>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 113;  
Best Local Similarity 93.8%; Pred. No. 8.3e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSRTRKNYL 16  
|||||:|||||  
Db 24 KSSQSLNSRTRKNYL 39

RESULT 7

G33932  
Ig kappa chain precursor V region (D23) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 21-Jan-2000  
C/Accession: G33932  
R/Baccala, R.; Vo Quang, T.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
A/Title: Two murine natural polypeptide autoantibodies are encoded by nonmutated germ-  
A/Reference number: A33932; PMID:89282823; PMID:2499867  
A/Accession: G33932  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-120 <BAC>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/36-116/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 72; DB 2; Length 120;  
Best Local Similarity 93.8%; Pred. No. 8.8e-06;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSQSLNSRTRKNYL 16  
|||||:|||||  
Db 44 KSSQSLNSRTRKNYL 59

RESULT 8

PH1050  
Ig light chain V region (clone 111-cl) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C/Accession: PH1050  
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1050  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-103 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 94.7%; Score 71; DB 2; Length 103;  
Best Local Similarity 93.8%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRKNTL 16  
DB 24 KSSQSLKSRTRKNTL 39  
|||||

RESULT 9  
PH101  
Ig light chain V region (clone 111.19) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1101  
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1101  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-104 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 94.7%; Score 71; DB 2; Length 104;  
Best Local Similarity 93.8%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRKNTL 16  
DB 24 KSSQSLKSRTRKNTL 39  
|||||

RESULT 10  
PH1102  
Ig light chain V region (clone 111.61) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1102  
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1102  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-104 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 94.7%; Score 71; DB 2; Length 104;  
Best Local Similarity 93.8%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRKNTL 16  
DB 24 KSSQSLKSRTRKNTL 39  
|||||

DB 24 KSSQSLKSRTRKNTL 39

RESULT 11  
PH1103  
Ig light chain V region (clone 111.109) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1103  
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1103  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-104 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 94.7%; Score 71; DB 2; Length 104;  
Best Local Similarity 93.8%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRKNTL 16  
DB 24 KSSQSLKSRTRKNTL 39  
|||||

RESULT 12  
PH1104  
Ig light chain V region (clone 111.100) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1104  
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1104  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-104 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 94.7%; Score 71; DB 2; Length 104;  
Best Local Similarity 93.8%; Pred. No. 1.2e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSQSLSSRRKNTL 16  
DB 24 KSSQSLKSRTRKNTL 39  
|||||

RESULT 13  
PL0265  
Ig kappa chain V region (anti-DNA, DP13VK and DP18VK) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
C:Accession: PL0265  
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pletschky, D.; Marshak-Rothstein, A  
J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
A:Reference number: PL0231; MUID:90111618; PMID:2104919  
A:Accession: PL0265  
A:Molecule type: mRNA  
A:Residues: 1-112 <SHL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Search completed: March 1, 2005, 17:44:46  
Job time : 22.6615 secs

C;Keywords: heterotrimer; immunoglobulin  
F;1-23/Region: framework 1  
F;16-96/Domain: immunoglobulin homology <IMM>  
F;24-40/Region: complementarity-determining 1  
F;41-55/Region: framework 2  
F;56-62/Region: complementarity-determining 2  
F;63-94/Region: framework 3  
F;95-102/Region: complementarity-determining 3  
F;103-112/Region: framework 4

Query Match 90.7%; Score 68; DB 2; Length 112;  
Best Local Similarity 87.5%; Pred. No. 4.4e-05;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSQSLSSRRTRKXYL 16  
|||:|||||  
Db 24 KSSQSLFNRRTRKXYL 39

## RESULT 14

PH1051 Ig light chain V region (clone 165.3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C;Accession: PH1051

R;Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1051

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-103 <rtl>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 67; DB 2; Length 103;  
Best Local Similarity 87.5%; Pred. No. 6.2e-05;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSQSLSSRRTRKXYL 16  
|||:|||||  
Db 24 KSSQSLNRRTRKXYL 39

## RESULT 15

PH1052 Ig light chain V region (clone 165.5) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C;Accession: PH1052

R;Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1052

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-103 <rtl>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 67; DB 2; Length 103;  
Best Local Similarity 87.5%; Pred. No. 6.2e-05;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSQSLSSRRTRKXYL 16  
|||:|||||  
Db 24 KSSQSLNRRTRKXYL 39

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 103.631 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-18  
Perfect score: 75  
Sequence: 1 KSSQSLSSRRKKNYL 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	84.0	255	2	O6KB05 mus musculi
2	50	66.7	121	1	KV40 HUMAN
3	50	66.7	133	1	KV4B HUMAN
4	50	66.7	134	1	KV4C HUMAN
5	49	65.3	114	1	KV4A HUMAN
6	47	62.7	109	1	KV4D HUMAN
7	46	61.3	687	2	O49728
8	44	58.7	396	1	AAT_ECOLI
9	44	58.7	396	1	AAT_SALTI
10	44	58.7	396	1	AAT_SALTY
11	44	58.7	396	2	O7N625
12	44	58.7	396	2	O8F939
13	44	58.7	396	2	O831N4
14	44	58.7	396	2	O8XDF3
15	44	58.7	396	2	O8XDF3
16	42	56.0	333	2	O6KCL8
17	42	56.0	358	2	O8EUG4
18	42	56.0	572	2	O61FZ6
19	41	54.7	216	2	O9CGK7
20	41	54.7	519	2	O61G01
21	41	54.7	624	2	O8HHY2
22	41	54.7	792	2	O6XK1
23	40	53.3	106	2	O82561
24	40	53.3	336	2	O16329
25	40	53.3	336	2	O16330
26	40	53.3	396	2	O8RND0
27	40	53.3	397	2	O8YV63
28	40	53.3	397	2	O9K0P5
29	40	53.3	398	2	O7QMD9
30	40	53.3	433	2	O6LYX4
31	40	53.3	656	2	O7NMG8

32	40	53.3	656	2	O8D4W4
33	40	53.3	657	2	O72P01
34	40	53.3	657	2	O8F7G0
35	40	53.3	1212	2	O7X5Q3
36	40	53.3	1216	2	O7X5P8
37	40	53.3	1216	2	O7X5Q0
38	40	53.3	1216	2	O7X5Q4
39	40	53.3	1216	2	O7X5Q7
40	40	53.3	1216	2	O7X5Q8
41	40	53.3	1216	2	O7X5Q9
42	40	53.3	1216	2	O7X5R0
43	40	53.3	3007	2	O14215
44	40	53.3	6669	1	NEBU HUMAN
45	39	52.0	47	1	RL34_WIGBR

## ALIGNMENTS

RESULT 1									
ID	Q6KB05	PRELIMINARY	PRT	255 AA.					
AC	O6KB05	05-JUL-2004 (TRENBLrel. 27, Created)							
DT	05-JUL-2004 (TRENBLrel. 27, Last sequence update)								
DE	05-JUL-2004 (TRENBLrel. 27, Last annotation update)								
GN	ScFv BB5 protein (Fragment).								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Balb/c.								
RA	Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,								
RL	Briand J.P., Hoebeke J.,								
DR	Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.								
DR	EMBL: AJ746180; CACB4081.1; -.								
DR	HSSP; P01837; IKCR.								
DR	InterPro; IPR003599; IG.								
DR	InterPro; IPR007110; IG_1like.								
DR	InterPro; IPR003596; IG_v.								
DR	SMART; SM00409; IG; 2.								
DR	SMART; SM00406; IGV; 2.								
DR	PROSITE; PS50835; IG LIKE; 2.								
FT	NON_TER								
FT	SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;								
Query Match									
		Best Local Similarity	84.0%;	Score 63;	DB 2;	Length 255;			
		Matches 13;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;			
OY	1 KSSQSLSSRRKKNYL 16	: :							
DB	160 KSSQSLSSRRKKNYL 175	: :							
RESULT 2									
ID	KV40 HUMAN	STANDARD;	PRT;	121 AA.					
AC	P06312;								
DT	01-JAN-1988 (Rel. 06, Created)								
DT	01-JAN-1988 (Rel. 06, Last sequence update)								
DT	05-JUL-2004 (Rel. 44, Last annotation update)								
DE	IG kappa chain V-IV region precursor (Fragment).								
GN	Name=IGKV4-1;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.								
OX	NCBI_Taxid=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								

```

RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlentz H.D.,
RA Zschau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
CC -I- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC -----
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CC -----
DR EMBL; Z00023; CAA77318.1; -.
DR PIR; A01902; K4HU.
DR HSSP; P01625; 1LVE.
DR Genew; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 >121
FT DOMAIN 21 43 Ig kappa chain V-IV region.
FT DOMAIN 44 60 Framework-1.
FT DOMAIN 61 75 Complementarity-determining-1.
FT DOMAIN 76 82 Framework-2.
FT DOMAIN 83 82 Complementarity-determining-2.
FT DOMAIN 115 122 Framework-3.
FT DOMAIN 114 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4180D33974 CRC64;

Query Match 66.7%; Score 50; DB 1; Length 121;
Best Local Similarity 68.8%; Pred. No. 0.37;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KSSQSLSRTRKRYL 16
DB 44 KSSQSVLYSSNNKYL 59

RESULT 3
KV4B_HUMAN STANDARD; PRT; 133 AA.
ID P06313;
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlentz H.D.,
RA Zschau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
DR EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HU1.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 133
FT DOMAIN 21 43 Ig kappa chain V-IV region JI.
FT DOMAIN 44 60 Framework-1.
FT DOMAIN 61 75 Complementarity-determining-1.
FT DOMAIN 76 82 Framework-2.
FT DOMAIN 83 82 Complementarity-determining-2.
FT DOMAIN 115 122 Framework-3.
FT DOMAIN 114 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON_TER 121 121
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 66.7%; Score 50; DB 1; Length 133;
Best Local Similarity 68.8%; Pred. No. 0.41;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KSSQSLSRTRKRYL 16
DB 44 KSSQSVLYSSNNKYL 59

RESULT 4
KV4C_HUMAN STANDARD; PRT; 134 AA.
ID KV4C_HUMAN
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RA Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X02990; CAA26733.1; -.

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DR HSP; P01625; 1LVE.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-1-like.  
 DR InterPro; IPR003596; Ig-1-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 134 Ig kappa chain V-IV region B17.  
 FT DOMAIN 21 43 Framework-1.  
 FT DOMAIN 44 60 Complementarity-determining-1.  
 FT DOMAIN 61 75 Complementarity-determining-2.  
 FT DOMAIN 76 82 Complementarity-determining-3.  
 FT DOMAIN 83 114 Framework-3.  
 FT DOMAIN 115 121 Complementarity-determining-4.  
 FT DOMAIN 122 133 Framework-4.  
 FT DISULFID 43 114 By similarity.  
 FT NON\_TER 134 134  
 SQ SEQUENCE 134 AA; 14966 MM; 6413A22FD0738832 CRC64;  
 Query Match 66.7%; Score 50; DB 1; Length 134;  
 Best Local Similarity 68.8%; Pred. No. 0.41;  
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KSSQSLSSRTKNTL 16  
 DB 44 KSSQSLVSSDNKNTL 59

## RESULT 5

KV4A\_HUMAN STANDARD; PRT; 114 AA.  
 AC P01625;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ig kappa chain V-IV region Len.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76004342; PubMed=50995;  
 RA Schneider M., Hilschmann N.;  
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
 RT subgroup IV of the kappa type (Bence-Jones protein Len).";  
 RT Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
 RL [2]  
 RP REVISION TO 9.  
 RA Salomon A.;  
 RL Submitted (AUG-1996) to Swiss-Prot.  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PDB; 1EEQ; X-ray; A/B=1-114.  
 DR PDB; 1EFQ; X-ray; A/B=1-114.  
 DR PDB; 1EK3; X-ray; A/B=1-114.  
 DR PDB; 1LVE; X-ray; @=1-114.  
 DR PDB; 1LVE; X-ray; @=1-114.  
 DR PDB; 3LVE; X-ray; A=1-114.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM 3d-structure; Bence-Jones protein; Direct protein sequencing;

KM Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 40 Complementarity-determining-1.  
 FT DOMAIN 41 55 Framework-2.  
 FT DOMAIN 56 62 Complementarity-determining-2.  
 FT DOMAIN 63 94 Framework-3.  
 FT DOMAIN 95 101 Complementarity-determining-3.  
 FT DOMAIN 102 113 Framework-4.  
 FT DISULFID 23 94 By similarity.  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT STRAND 30 31  
 FT TURN 32 35  
 FT STRAND 36 37  
 FT STRAND 39 44  
 FT TURN 46 47  
 FT STRAND 51 55  
 FT TURN 56 58  
 FT STRAND 59 60  
 FT TURN 62 63  
 FT TURN 66 67  
 FT STRAND 68 73  
 FT TURN 74 75  
 FT STRAND 76 81  
 FT HELIX 86 88  
 FT STRAND 90 96  
 FT STRAND 103 104  
 FT STRAND 108 112  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12640 MM; 0647F1D17F236485 CRC64;  
 Query Match 65.3%; Score 49; DB 1; Length 114;  
 Best Local Similarity 68.8%; Pred. No. 0.52;  
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KSSQSLSSRTKNTL 16  
 DB 24 KSSQSLVSSDNKNTL 39

## RESULT 6

KV4D\_HUMAN STANDARD; PRT; 109 AA.  
 AC P83593;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-IV region 5TH (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Abdominal adipose tissue;  
 RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/birc.1998.8515;  
 RA Olsen K.E., Sletten K., Westermarck P.;  
 RT "Extended analysis of AL-amyloid protein from abdominal wall  
 RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";  
 RT Biochem. Biophys. Res. Commun. 245:713-716(1998).  
 CC -1- FUNCTION: May play an important role in fibrillogenesis.  
 DR InterPro; IPR007110; Ig-1-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Direct protein sequencing; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 40 Complementarity-determining-1.  
 FT DOMAIN 41 55 Framework-2.  
 FT DOMAIN 56 62 Complementarity-determining-2.

FT DOMAIN 63 94 Framework-3.  
 FT DOMAIN 95 101 Complementarity-determining-3.  
 FT DOMAIN 102 109 Framework-4.  
 FT DISUPID 23 94 By similarity.  
 FT UNSURE 23 23  
 FT UNSURE 94 94  
 FT NON TER 109 109  
 SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;  
 Query Match 62.7%; Score 47; DB 1; Length 109;  
 Best Local Similarity 62.5%; Pred. No. 1.2;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 KSSQSLSSRTKRYL 16  
 Db 24 RSSQSVLYSSNNKNYL 39  
 RESULT 7  
 ID 049728 PRELIMINARY; PRT; 687 AA.  
 AC 049728;  
 DT 01-JUN-1998 (TEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
 DE Receptor serine/threonine kinase-like protein.  
 GN Name=TA21.100; Synonyms=AT4G18280;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxId=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,  
 RA Mayer K.F.X., Lemcke K., Scheller C.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL: AL021713; CA16797.1; -;  
 DR EMBL: AL161548; CAB78627.1; -;  
 DR PIR: T04927; T04927.  
 DR HSSP: P02883; IRQM.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0016740; F:transferase activity; IEA.  
 DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR011009; Kinase\_like.  
 DR InterPro: IPR008271; Ser Thr pkin\_AS.  
 DR InterPro: IPR001938; Thaumatin.  
 DR Pfam: PF00314; Thaumatin; 2.  
 DR ProDom: PD000001; Prot\_Kinase; 1.  
 DR ProDom: PD001321; Thaumatin; 2.  
 DR SMART: SM00205; THN; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00108; PROTEIN KINASE STM; 1.  
 DR PROSITE: PS00316; THAUMATIN; UNKNOWN; 1.  
 KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;  
 Transferase.

SQ SEQUENCE 687 AA; 77096 MW; 3D2E57112AF2C84 CRC64;  
 Query Match 61.3%; Score 46; DB 2; Length 687;  
 Best Local Similarity 64.3%; Pred. No. 16;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 SSQSLSSRTKRYL 15  
 Db 667 STQSLERKTRSNV 680  
 RESULT 8  
 AAT\_ECOLI  
 ID AAT\_ECOLI STANDARD; PRT; 396 AA.  
 AC P00509;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 25-JUN-2005 (Rel. 46, Last annotation update)  
 DE Aspartate aminotransferase (EC 2.6.1.1) (transaminase A) (ASPART).  
 GN Name=aspC; OrderedLocustNames=b0928;  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI\_TaxId=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85289110; PubMed=3897210;  
 RA Kuratlew S., Okuno S., Ogawa T., Ogawa H., Kagamiyama H.;  
 RT "Aspartate aminotransferase of Escherichia coli: nucleotide sequence  
 of the aspC gene.";  
 RL J. Biochem. 97:1259-1262(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8624211; PubMed=3521591;  
 RA Rotheringham I.G., Dacey S.A., Taylor P.P., Smith T.J., Hunter M.G.,  
 RA Finlay M.E., Primrose S.B., Parker D.M., Edwards R.M.;  
 RT "The cloning and sequence analysis of the aspC and tyrB genes from  
 Escherichia coli K12. Comparison of the primary structures of the  
 RT aspartate aminotransferase and aromatic aminotransferase of E. coli  
 RT with those of the pig aspartate aminotransferase isoenzymes.";  
 RL Biochem. J. 234:593-604(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / M61655;  
 RX MEDLINE=9746617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Alba H., Baba T., Fujita K., Hayaishi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kasubuchi K.,  
 RA Kimura S., Kitagawa M., Makino K., Maeda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Naeshimoto H., Nishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.;  
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155(1996).  
 RN [5]  
 RP SEQUENCE.  
 RX MEDLINE=84256832; PubMed=6378205;  
 RA Kondo K., Wakabayashi S., Yagi T., Kagamiyama H.;  
 RT "The complete amino acid sequence of aspartate aminotransferase from  
 RT Escherichia coli: sequence comparison with pig isoenzymes.";  
 RL Biochem. Biophys. Res. Commun. 122:62-67(1984).  
 RN [6]  
 RP SEQUENCE.

RX MEDLINE=87250482; PubMed=3298240;  
 RA Kondo K., Wakabayashi S., Kagamiyama H.;  
 RT "Structural studies on aspartate aminotransferase from Escherichia  
 coli. Covalent structure.";  
 RL J. Biol. Chem. 262:8648-8659 (1987).  
 RN [7]  
 RP SEQUENCE OF 1-12.  
 RC STRAIN=K12 / EMG2;  
 RX MEDLINE=97443975; PubMed=9298646;  
 RA Link A.J., Robison K., Church G.M.;  
 RT "Comparing the predicted and observed properties of proteins encoded  
 in the genome of Escherichia coli K-12.";  
 RL Electrophoresis 18:1259-1313 (1997).  
 RN [8]  
 RP MUTAGENESIS OF TYR-65.  
 RX MEDLINE=91329346; PubMed=1868057;  
 RA Inoue K., Kuramitsu S., Okamoto A., Hirotsu K., Higuchi T.,  
 Kagamiyama H.;  
 RT "Site-directed mutagenesis of Escherichia coli aspartate  
 aminotransferase: role of Tyr70 in the catalytic processes.";  
 RL Biochemistry 30:7796-7801 (1991).  
 RN [9]  
 RP MUTAGENESIS OF HIS-133.  
 RX MEDLINE=91177849; PubMed=2007566;  
 RA Yano T., Kuramitsu S., Tanase S., Morino Y., Hiroshi K., Kagamiyama H.;  
 RT "The role of His143 in the catalytic mechanism of Escherichia coli  
 aspartate aminotransferase.";  
 RL J. Biol. Chem. 266:6079-6085 (1991).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF MUTANT ALA-246.  
 RX MEDLINE=90105323; PubMed=2513875;  
 RA Smith D.L., Almo S.C., Toney M.D., Range D.;  
 RT "2.8-A-resolution crystal structure of an active-site mutant of  
 aspartate aminotransferase from Escherichia coli.";  
 RL Biochemistry 28:8161-8177 (1989).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS), AND MUTAGENESIS OF ARG-374.  
 RX MEDLINE=91129283; PubMed=1993208;  
 RA Danilnefsky A.T., Ommer J.J., Petsko G.A., Range D.;  
 RT "Activity and structure of the active-site mutants R366Y and R386F of  
 Escherichia coli aspartate aminotransferase.";  
 RL Biochemistry 30:1980-1985 (1991).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF MUTANT.  
 RX MEDLINE=99107891; PubMed=9891001; DOI=10.1074/jbc.274.4.2344;  
 RA Oue S., Okamoto A., Yano T., Kagamiyama H.;  
 RT "Redesigning the substrate specificity of an enzyme by cumulative  
 effects of the mutations of non-active site residues.";  
 RL J. Biol. Chem. 274:2344-2349 (1999).  
 CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +  
 L-glutamate.  
 CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent  
 aminotransferase family.  
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 CC  
 CC EMBL: X03629; CAA27279.1; -;  
 CC EMBL: X05904; CAA29333.1; -;  
 CC EMBL: U00096; AAC74014.1; -;  
 CC EMBL: D90730; BAA35674.1; -;  
 CC EMBL: D90731; BAA35680.1; -;  
 CC PIR: A00598; XNECD.  
 CC PDB: 1AAM; X-ray; @=1-396.  
 CC PDB: 1AAW; X-ray; @=1-396.

DR PDB: 1AHE; X-ray; A/B=1-396.  
 DR PDB: 1AHF; X-ray; A/B=1-396.  
 DR PDB: 1AHG; X-ray; A/B=1-396.  
 DR PDB: 1AHX; X-ray; A/B=1-396.  
 DR PDB: 1AHY; X-ray; A/B=1-396.  
 DR PDB: 1AIA; X-ray; A/B=1-396.  
 DR PDB: 1AIB; X-ray; A/B=1-396.  
 DR PDB: 1AIC; X-ray; A/B=1-396.  
 DR PDB: 1AMQ; X-ray; @=1-396.  
 DR PDB: 1AMR; X-ray; @=1-396.  
 DR PDB: 1AMS; X-ray; @=1-396.  
 DR PDB: 1AKG; X-ray; A/B=1-396.  
 DR PDB: 1ARH; X-ray; A/B=1-396.  
 DR PDB: 1ARI; X-ray; A/B=1-396.  
 DR PDB: 1ART; X-ray; @=1-396.  
 DR PDB: 1ASA; X-ray; @=1-396.  
 DR PDB: 1ASB; X-ray; @=1-396.  
 DR PDB: 1ASC; X-ray; @=1-396.  
 DR PDB: 1ASD; X-ray; @=1-396.  
 DR PDB: 1ASE; X-ray; @=1-396.  
 DR PDB: 1ASF; X-ray; @=1-396.  
 DR PDB: 1ASG; X-ray; @=1-396.  
 DR PDB: 1ASL; X-ray; A/B=1-396.  
 DR PDB: 1ASM; X-ray; A/B=1-396.  
 DR PDB: 1ASN; X-ray; A/B=1-396.  
 DR PDB: 1B4X; X-ray; A=1-396.  
 DR PDB: 1BQA; X-ray; A/B=1-396.  
 DR PDB: 1BQD; X-ray; A/B=1-396.  
 DR PDB: 1C9C; X-ray; A=1-396.  
 DR PDB: 1C9Q; X-ray; A=1-396.  
 DR PDB: 1CQ6; X-ray; A=1-396.  
 DR PDB: 1CQ7; X-ray; A=1-396.  
 DR PDB: 1CQ8; X-ray; A=1-396.  
 DR PDB: 1CZC; X-ray; A=1-396.  
 DR PDB: 1CZE; X-ray; A=1-396.  
 DR PDB: 1G4V; X-ray; A=1-396.  
 DR PDB: 1G4W; X-ray; A=1-396.  
 DR PDB: 1G7X; X-ray; A=1-396.  
 DR PDB: 1IX6; X-ray; A=1-396.  
 DR PDB: 1IX7; X-ray; A=1-396.  
 DR PDB: 1IX8; X-ray; A=1-396.  
 DR PDB: 1QIR; X-ray; A=1-396.  
 DR PDB: 1QIS; X-ray; A=1-396.  
 DR PDB: 1QIT; X-ray; A=1-396.  
 DR PDB: 1SPA; X-ray; @=1-396.  
 DR PDB: 1YOO; X-ray; @=1-396.  
 DR PDB: 2AAT; X-ray; @=1-396.  
 DR PDB: 2AAT; X-ray; @=1-396.  
 DR PDB: 2BAA; X-ray; A=1-396.  
 DR SWISS-2DPAGE; P00509; COLI.  
 DR EC02DBASE; F039.6; 6TH EDITION.  
 DR EC02DBASE; F039.7; 6TH EDITION.  
 DR ECHOBASE; EB0094; -;  
 DR EcGene; EG10096; aapC.  
 DR InterPro; IPR004839; Aminotrans\_I/II.  
 DR InterPro; IPR00796; Asp\_trans.  
 DR InterPro; IPR004838; Nhltransf\_1\_BS.  
 DR Pfam; PF00155; Aminotran\_1\_2; 1.  
 DR PRINTS; PR00799; TRANSAMINSE.  
 DR PROSITE; PS00105; AA\_TRANSFER CLASS.1; 1.  
 KW 3D-structure; Aminotransferase; Complete proteome;  
 KW Direct protein sequencing; Pyridoxal phosphate; Transferease.  
 FT BINDING 246  
 FT ACT SITE 374  
 FT MUTAGEN 133

Query Match 58.7%; Score 44; DB 1; Length 396;  
 Best Local Similarity 56.2%; Pred. NO. 19;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 KSSQSLSSRRTRKNYL 16

Db 51 KAEQYLLNETTKNYL 66

## RESULT 9

AAT\_SALTY ID AAT\_SALTY STANDARD; PRT; 396 AA.  
AC 056114;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (aspart).  
GN Name=aspC; OrderedLocustNames=STY1000, t1936;  
OS Salmonella typhi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=601;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;  
RA Churchill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
Feltwell T., Hamlin N., Haque A., Hien T.T., Holtz S., Jagels K.,  
Koch A., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,  
Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,  
Whitehead S., Barrett B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
enterica serovar Typhi CT18."  
RL Nature 413:848-852(2001).  
RN 12  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12644504;  
DOI=10.1128/JB.185.7.2330-2337.2003;  
RA Deng W., Lion S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;  
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
and CT18."  
RL J. Bacteriol. 185:2330-2337(2003).  
RN 13  
RP SEQUENCE OF 1-74 FROM N.A.  
RC STRAIN=IMSS-1;  
RA Fernandez-Mora M., Calva E.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +  
L-glutamate.  
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent  
aminotransferase family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC  
CC EMBL; AL627268; CAD05398.1; -  
DR EMBL; AEO16840; AA069551.1; -  
DR EMBL; X89757; CA61906.1; -  
DR HSSP; P00509; 1ART.  
DR InterPro; IPR004839; Aminotrans\_I/II.  
DR InterPro; IPR000796; Asp\_trans.  
DR InterPro; IPR004838; NHTransf\_1\_BS.  
DR Pfam; PF00155; Aminotran\_1\_2; 1.  
DR PRINTS; PR00799; TRANSAMINASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.

KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.  
FT BINDING 246 246 Pyridoxal phosphate (By similarity).  
FT ACT SITE 374 374  
SQ SEQUENCE 396 AA; 43507 MW; 974C158543BD02FB CRC64;

Query Match 58.7%; Score 44; DB 1; Length 396;  
Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 KSSQSLSSRTKRYL 16  
Db 51 KAEQYLLNETTKNYL 66

## RESULT 10

AAT\_SALTY ID AAT\_SALTY STANDARD; PRT; 396 AA.  
AC P58661;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (aspart).  
GN Name=aspC; OrderedLocustNames=STW0998;  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=602;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=L72 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;  
RA McLelland M., Sanderson K.E., Spiegh J., Clifton S.W., Latreille P.,  
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
Ryan E., Sun H., Flores L., Miller W., Stoecking T., Nman M.,  
Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
L72."  
RL Nature 413:852-856(2001).  
RN 12  
RP SEQUENCE OF 1-74 FROM N.A.  
RC STRAIN=IMSS-1;  
RA Fernandez-Mora M., Calva E.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +  
L-glutamate.  
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent  
aminotransferase family.  
CC  
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CC  
CC EMBL; AEO08743; AAL19932.1; -  
DR HSSP; P00509; 1ART.  
DR StryGene; SG77777; aspc.  
DR InterPro; IPR004839; Aminotrans\_I/II.  
DR InterPro; IPR000796; Asp\_trans.  
DR InterPro; IPR004838; NHTransf\_1\_BS.  
DR Pfam; PF00155; Aminotran\_1\_2; 1.  
DR PRINTS; PR00799; TRANSAMINASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
DR Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.  
FT BINDING 246 246 Pyridoxal phosphate (By similarity).  
FT ACT SITE 374 374  
SQ SEQUENCE 396 AA; 43521 MW; 960940D0148D02FB CRC64;  
QY  
Query Match 58.7%; Score 44; DB 1; Length 396;  
Best Local Similarity 56.2%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 KSSQSLSSRTKXNYL 16
      ||| : |||
      51 KAEQYLENETTKNYL 66

Db
RESULT 11
ID Q7N625 PRELIMINARY: PRT; 396 AA.
AC Q7N625:
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Aspartate aminotransferase (Transaminase A).
GN Name=aspc; OrderedlocusNames=plu1750;
OS Photorhabdus luminescens (subsp. laumondii);
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TT01;
RA MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusnlok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Bude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudreault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.,
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RT RL Biotechnol. 21:1307-1313 (2003).
DR EMBL; BX571864; CAE14043.1; -.
DR HSSP; P00509; IART.
DR Photocist: plu1750; -.
DR GO; GO:000483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:amino acid metabolism; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR InterPro; IPR004839; Aminotransf_1/I.
DR InterPro; IPR00796; Asp_trans_1_BS.
DR InterPro; IPR004838; Nitransf_1_BS.
DR Pfam; PF00155; Aminotran_1_2; 1.
DR PRINTS; PR00799; TRANSAMINASE.
DR PROSITE; PS00105; AA TRANSFER CLASS 1; 1.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 396 AA; 43575 MW; 7EC3E64A6DBC26 CRC64;

Query Match      58.7%; Score 44; DB 2; Length 396;
Best Local Similarity 56.2%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 KSSQSLSSRTKXNYL 16
      ||| : |||
      51 KAEQYLENETTKNYL 66

Db
RESULT 12
ID Q8FJ99 PRELIMINARY: PRT; 396 AA.
AC Q8FJ99:
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Aspartate aminotransferase (EC 2.6.1.1).
GN Name=aspc; OrderedlocusNames=ct1070;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CPT073 / ATCC 700928 / UPEC;
RX MEDLINE=2238834; PubMed=12471157; DOI=10.1073/pnas.252529799;
RX Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

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RA Raeko D., Buckles E.L., Liu S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Domenech M.S., Blatner F.R., Perna N.T.,
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RT Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016758; AAN79538.1; -.
DR HSSP; P00509; IART.
DR GO; GO:0004069; F:aspartate transaminase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR InterPro; IPR004839; Aminotrans_1/I.
DR InterPro; IPR00796; Asp_trans_1/I.
DR InterPro; IPR004838; Nitransf_1_BS.
DR Pfam; PF00155; Aminotran_1_2; 1.
DR PRINTS; PR00799; TRANSAMINASE.
DR PROSITE; PS00105; AA TRANSFER CLASS 1; 1.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 396 AA; 43568 MW; 9F4A6EC8A13FC679 CRC64;

Query Match      58.7%; Score 44; DB 2; Length 396;
Best Local Similarity 56.2%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 KSSQSLSSRTKXNYL 16
      ||| : |||
      51 KAEQYLENETTKNYL 66

Db
RESULT 13
ID Q83LN4 PRELIMINARY: PRT; 396 AA.
AC Q83LN4; Q7C286;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Aspartate aminotransferase.
GN Name=aspc; OrderedlocusNames=80989, SF0925;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RX Jin Q., Yan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RX Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RX Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RX Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RX Yu J.,
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RT Nucleic Acids Res. 30:4432-4441 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RX Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RX Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RX Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RX Schwartz D.C., Blatner F.R.,
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RT Infect. Immun. 71:2775-2786 (2003).
DR EMBL; AE015122; AAN4254.1; -.
DR EMBL; AE016981; AAP16440.1; -.
DR HSSP; P00509; IART.
DR GO; GO:0004843; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.

```

DR InterPro: IPR004839; AminoTrans\_I/II.  
 DR InterPro: IPR000796; Asp\_trans.  
 DR InterPro: IPR004838; NHTransf\_1\_BS.  
 DR Pfam: PF00155; AminoTrans\_1\_2\_1.  
 DR PRINTS: PR00799; TRANSAMINASE.  
 DR PROSITE: PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
 DR AminoTransferase; Transferase; Complete proteome.  
 KW SEQUENCE 396 AA; 43617 MW; 621C1FB9FBA4DD5A CRC64;

Query Match 58.7%; Score 44; DB 2; Length 396;  
 Best Local Similarity 56.2%; Pred. No. 19;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTTRKYL 16  
 | : | | : | | | |  
 Db 51 KAEQYLENETTKNYL 66

## RESULT 14

Q8XDF3 PRELIMINARY; PRT; 396 AA.

AC Q8XDF3 07AG50; PRT; 396 AA.  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Apatate amino transferase.  
 GN Name: aspc; Ordered locus names: EC61011, z1275;  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;  
 RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;  
 RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobleck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.,  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7,"  
 RL Nature 409:529-533(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takemi H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12,"  
 RL DNA Res. 8:11-22(2001).  
 DR EMBL: AB005282; AAG55413.1; -.  
 DR EMBL: AP002553; BAB34434.1; -.  
 DR PIR: A85619; A85619.  
 DR PIR: C90755; C90755.  
 DR HSSP: P00509; IART.  
 DR GO: GO:0008483; F:transaminase activity; IEA.  
 DR GO: GO:0016740; F:transferase activity; IEA.  
 DR GO: GO:0006520; P:amino acid metabolism; IEA.  
 DR GO: GO:0009058; P:biosynthesis; IEA.  
 DR InterPro: IPR004839; AminoTrans\_I/II.  
 DR InterPro: IPR000796; Asp\_trans.  
 DR InterPro: IPR004838; NHTransf\_1\_BS.  
 DR Pfam: PF00155; AminoTrans\_1\_2\_1.  
 DR PRINTS: PR00799; TRANSAMINASE.  
 DR PROSITE: PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
 KW AminoTransferase; Transferase; Complete proteome.  
 SQ SEQUENCE 396 AA; 43645 MW; 81C2063CE24DF08 CRC64;

Query Match 58.7%; Score 44; DB 2; Length 396;

Best Local Similarity 56.2%; Pred. No. 19;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTTRKYL 16  
 | : | | : | | | |  
 Db 51 KAEQYLENETTKNYL 66

## RESULT 15

Q6MCL8 PRELIMINARY; PRT; 333 AA.

AC Q6MCL8  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN Order: locus names: pc0957;  
 OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).  
 OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.  
 OX NCBI\_TaxID=264201;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Burkhold U.,  
 RA Fairman B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
 RA Rattei T., Mewes H.-W., Wagner M.;  
 RT "Genome sequence of an amoeba symbiont and its use for reconstructing  
 the evolutionary history of chlamydiae,"  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BX908798; CAP23681.1; -.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 333 AA; 39257 MW; 6C88A8B88C85D816 CRC64;

Query Match 56.0%; Score 42; DB 2; Length 333;  
 Best Local Similarity 53.3%; Pred. No. 37;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KSSQSLSSRTTRKYL 15  
 | : | | : | | | |  
 Db 16 EDKSLTTRIRKYL 30

Search completed: March 1, 2005, 17:43:17  
 Job time: 105.631 secs

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# OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 52.3385 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-19  
Perfect score: 38  
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

## Database :

A: Geneseqp\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	2	AAR30157 MAB GAH v
2	38	100.0	7	2	AAR57966 MAB NFS2
3	38	100.0	7	2	AAR50317 MAB NFS2
4	38	100.0	7	2	AAR57964 MAB NFS2
5	38	100.0	7	2	AAV08713 Human m1
6	38	100.0	7	3	AAV95234 Human mon
7	38	100.0	7	3	AAV32227 G-CSF ago
8	38	100.0	7	3	AAB07952 CDR2 sequ
9	38	100.0	7	5	AAU81257 Human trk
10	38	100.0	7	5	AAB62361 Human imm
11	38	100.0	7	5	AAB29275 Anti-CL1a
12	38	100.0	7	5	ABG68854 CDR2 VL p
13	38	100.0	7	5	AAU70347 Mouse Kap
14	38	100.0	7	5	AAU70335 Human Kap
15	38	100.0	7	6	AAE34369 Escherich
16	38	100.0	7	6	ABP98689 Human GAH
17	38	100.0	7	6	ABP98681 Human GAH
18	38	100.0	7	6	ABG71653 CDR2 of H
19	38	100.0	7	6	AAE38110 Human COU
20	38	100.0	7	7	ABO33872 Anti-GPI-
21	38	100.0	7	7	ABO33869 Anti-GPI-
22	38	100.0	7	7	ADC97709 Mouse mon
23	38	100.0	7	7	ADG43867 Human pep
24	38	100.0	7	8	ADL23027 Myelin as
25	38	100.0	7	8	ADO32089 Mouse ant

26	38	100.0	7	8	ADO58066 S2 cell d
27	38	100.0	7	8	ADP47268 Human pho
28	38	100.0	7	8	ADP47250 Human pho
29	38	100.0	7	8	ADP47241 Human pho
30	38	100.0	7	8	ADP47271 Human pho
31	38	100.0	7	8	ADP47286 Human pho
32	38	100.0	7	8	ADO28264 Method of
33	38	100.0	7	8	ADO88787 Light cha
34	38	100.0	12	8	ADO32134 Mouse ant
35	38	100.0	15	5	ABG68859 CDR2 sequ
36	38	100.0	17	8	ADR38445 Human N-t
37	38	100.0	82	2	AAW62807 Amino aci
38	38	100.0	84	2	AAW14491 Monoclon
39	38	100.0	84	2	AAW99878 Monoclon
40	38	100.0	94	3	AAV56669 Partial p
41	38	100.0	98	7	ADC99827 Anti-huma
42	38	100.0	98	7	ADD05431 Anti-MUC1
43	38	100.0	98	7	ADF09869 Anti-MUC1
44	38	100.0	99	8	ADO32144 Mouse ant
45	38	100.0	101	6	ABJ18696 Antibody

## ALIGNMENTS

RESULT 1	AAAR30157	standard; protein; 7 AA.
ID	AAAR30157	
AC	AAAR30157;	
XX		
DT	25-MAR-2003 (revised)	
DT	06-MAY-1993 (first entry)	
DE	MAB GAH variable region of light chain.	
KW	Monoclonal antibody; hybridoma; PCR; variable region; constant region; heavy chain; light chain.	
OS	Synthetic.	
PN	EP520499-A1.	
PD	30-DEC-1992.	
PF	26-JUN-1992; 92EP-00110841.	
PR	28-JUN-1991; 91JP-00158859.	
PR	28-JUN-1991; 91JP-00158860.	
PR	28-JUN-1991; 91JP-00158861.	
XX		
XX	(MITU ) MITSUBISHI KASEI CORP.	
PI	Hosokawa S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;	
XX	WPI; 1993-001328/01.	
DR	N-PSDB; AAQ33044.	
PT	Human monoclonal antibody specific for a cancer cell membrane surface antigen - prepd. from a hybridoma obtd. by cell fusion between human lymphocytes derived from cancer patients and mouse myeloma cells.	
PT	Claim 3; Page 30 + 23; 37pp; English.	
PS	The sequence is described is the specification as having 27 bases. A human Mab specifically binding to a surface antigen of cancer cell membrane comprises variable regions of the heavy and light chains having the amino acid sequences of AAR30153-55 and AAR30156-58 respectively, encoded by DNA sequences AAQ33040-42 and AAQ33043-45 respectively. The antibody is obtained from a hybridoma producing human antibody GAH. (Updated on 25-MAR-2003 to correct PN field.)	
CC	Sequence 7 AA:	
XX		
SO		

Query Match 100.0%; Score 38; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
 |||||  
 Db 1 WASTRES 7

## RESULT 2

AAR57966 standard; protein; 7 AA.

AC AAR57966;

DT 25-MAR-2003 (revised)  
 DT 05-OCT-1994 (first entry)

DE MAb NFS2 light chain variable region CDR2 (modified).

XX Monoclonal antibody; Plasmodium falciparum; CDR;

KM complementarity determining region; fusion protein; murine; variable;  
 KM light; heavy; chain; malaria.

XX Synthetic.

XX WO9405690-A1.

PD 17-MAR-1994.

PF 08-SEP-1993; 93WO-US008435.

PR 09-SEP-1992; 92US-00941654.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (USNA ) US SEC OF NAVY.

PA (USSA ) US SEC OF ARMY.

XX Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;

PI Charenevlt Y, Hurtle M;

DR WPI; 1994-101115/12.

XX N-PSDB; AAQ44839.

XX New engineered antibodies and fusion proteins for preventing Plasmodium

PT infection - contg. murine antibody CDR sequences, and corresp. nucleic

PT acid, vectors and transformed cells.

XX Disclosure; Page 69; 98pp; English.

XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable

CC light chain and variable heavy chain sequences derived from murine mAb

CC NFS2 are provided. Murine mAb NFS2, its variable chain peptides, CDRs,

CC functional fragments, Fab fragments, and analogs are useful in prodn. of

CC fusion proteins, esp. engineered antibodies. These prods. are used to

CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to

CC correct PN field.)

XX Sequence 7 AA;

XX Query Match 100.0%; Score 38; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
 |||||  
 Db 1 WASTRES 7

## RESULT 3

AAR50317 standard; protein; 7 AA.

XX AAR50317;  
 AC 25-MAR-2003 (revised)  
 DT 05-OCT-1994 (first entry)

XX MAb NFS2 light chain variable region CDR2 (modified).

XX Monoclonal antibody; Plasmodium falciparum; CDR;

KM complementarity determining region; fusion protein; murine; variable;  
 KM light; heavy; chain; malaria.

XX Synthetic.

XX WO9405690-A1.

PD 17-MAR-1994.

PF 08-SEP-1993; 93WO-US008435.

PR 09-SEP-1992; 92US-00941654.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (USNA ) US SEC OF NAVY.

PA (USSA ) US SEC OF ARMY.

XX Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;

PI Charenevlt Y, Hurtle M;

DR WPI; 1994-101115/12.

XX N-PSDB; AAQ44833.

XX New engineered antibodies and fusion proteins for preventing Plasmodium

PT infection - contg. murine antibody CDR sequences, and corresp. nucleic

PT acid, vectors and transformed cells.

XX Claim 16; Page 83; 98pp; English.

XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable

CC light chain and variable heavy chain sequences derived from murine mAb

CC NFS2 are provided. Murine mAb NFS2, its variable chain peptides, CDRs,

CC functional fragments, Fab fragments, and analogs are useful in prodn. of

CC fusion proteins, esp. engineered antibodies. These prods. are used to

CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to

CC correct PN field.)

XX Sequence 7 AA;

XX Query Match 100.0%; Score 38; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7  
 |||||  
 Db 1 WASTRES 7

XX MAb NFS2 light chain variable region CDR2.

XX Monoclonal antibody; Plasmodium falciparum; CDR;

KM complementarity determining region; fusion protein; murine; variable;  
 KM light; heavy; chain; malaria.

XX Plasmodium falciparum.

OS



XX WO9405690-A1.  
 PN  
 XX 17-MAR-1994.  
 PD  
 XX  
 XX 08-SEP-1993; 93WO-US008435.  
 PF  
 XX 09-SEP-1992; 92US-00941654.  
 PR  
 XX (SMK ) SMITHKLINE BEECHAM CORP.  
 PA (USNA ) US SEC OF NAVY.  
 PA (USNA ) US SEC OF ARMY.  
 XX  
 PI Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvestre DR;  
 PI Charoenaviv Y, Hurlle M;  
 XX WPI: 1994-101115/12.  
 DR N-PSDB; AAQ44837.  
 XX  
 PT New engineered antibodies and fusion proteins for preventing Plasmodium  
 PT infection - contg. murine antibody CDR sequences, and corresp. nucleic  
 PT acid, vectors and transformed cells.  
 XX  
 PS Disclosure; Page 68; 98pp; English.  
 XX  
 CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28) variable  
 CC light chain and variable heavy chain sequences derived from murine mab  
 CC NPS2 are provided. Murine mab NPS2, its variable chain peptides, CDRs,  
 CC functional fragments, Fab fragments, and analogs are useful in prodn. of  
 CC functional proteins, esp. engineered antibodies. These prods. are used to  
 CC protect humans against Plasmodium infections. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 |||||  
 Db 1 WASTRES 7

RESULT 5  
 AAY08713

ID AAY08713 standard; protein; 7 AA.

XX AC AAY08713;

XX DT 10-AUG-1999 (first entry)

XX DE Human milk fat globule antigen binding fragment 5.

XX KW Immunoglobulin; immunospecific; variable domain; CDR; cancer antigen;  
 KW complementarity determining region; infectious disease agent antigen;  
 KW cellular receptor; infectious agent; chemotherapeutic agent; vaccine;  
 KW cancer; infectious disease; autoimmune disease; rheumatoid arthritis;  
 KW ulcerative colitis; psoriasis; allergy; immunoassay reagent; diagnosis;  
 KW veterinary medicine; antibody; immunisation; antibody; immune tolerance;  
 KW human milk fat globule antigen; cryptic expression;  
 KW anti-idiotypic immune response.

XX OS Homo sapiens.

XX PN WO9925378-A1.

XX PD 27-MAY-1999.

XX PF 13-NOV-1998; 98WO-US024302.

XX PR 14-NOV-1997; 97US-0065716P.

XX PR 10-APR-1998; 98US-0081403P.

XX (EURO-) EUROCELLTIGUE SA.

XX PI Burch RM;

XX DR WPI: 1999-357555/30.

XX PT Modified immunoglobulins including engineered binding site.

XX PS Claim 9; Page 76; 123pp; English.

XX This invention describes a novel modified immunoglobulin (mig), or its  
 CC fragment, that binds immunospecifically to one member (M1) of a binding  
 CC pair comprising a variable domain (V) having at least one CDR  
 CC (complementarity determining region) that contains a portion of the  
 CC second member (M2) of the pair. This portion is not present in the  
 CC natural CDR and M1 is a cancer antigen, infectious disease agent antigen,  
 CC a cellular receptor for an infectious agent (provided the binding site is  
 CC not NAMP or NUDP) or a member of a receptor-ligand pair. mig (also  
 CC related molecules containing the same V region), optionally coupled to a  
 CC chemotherapeutic agent, are used in therapeutic and/or prophylactic  
 CC compositions, or vaccines, against cancers, infectious or autoimmune  
 CC diseases (rheumatoid arthritis, ulcerative colitis or psoriasis) or  
 CC allergies. They can also be used as immunoassay reagents for diagnosing  
 CC these conditions. mig can be used in human or veterinary medicine. mig  
 CC have higher affinity for specificity than native antibodies. Manipulation  
 CC of CDR ensures binding specificity and avoids the unpredictable  
 CC immunisation and screening procedures currently used. It is now possible  
 CC to generate antibodies against antigens that are inaccessible, by virtue  
 CC of immune tolerance or cryptic expression. mig neutralize antigens  
 CC directly or they induce an anti-idiotypic immune response. This sequence  
 CC represents a fragment of modified immunoglobulin that immunospecifically  
 CC binds to a binding pair in which the first member is the human milk fat  
 CC globule antigen

SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 |||||  
 Db 1 WASTRES 7

RESULT 6  
 AAY95234

ID AAY95234 standard; peptide; 7 AA.

XX AC AAY95234;

XX DT 29-AUG-2000 (first entry)

XX DE Human monoclonal antibody LEN VL CDR2.

XX KW Human; monoclonal antibody; LEN; humanised antibody; CC49; HuCC49; CDR;  
 KW complementarity determining region; colon cancer;  
 KW tumor associated glycoprotein-72; TAG-72; tumour marker; carcinoma;  
 KW diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key

XX FT Region 1..6 Location/Qualifiers  
 XX /note= "specificity determining region"

XX PN WO200026394-A1.

XX PD 11-MAY-2000.

XX PF 29-OCT-1999; 99WO-US025552.

PR 31-OCT-1998; 98US-0106534P.  
 PR 02-NOV-1998; 98US-0106757P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Kashmiri SVS, Padlan EA, Schlom J;  
 DR WPI; 2000-365637/31.  
 XX  
 PT Chimeric variants of CC49 monoclonal antibodies useful for detecting and  
 PT treating cancers associated with the expression of the pancreaticoma tumor  
 PT -associated antigen TAG-72.  
 XX  
 XX Disclosure; Fig 2; 76pp; English.  
 XX  
 CC The present sequence is that of complementarity determining region 2 (L-  
 CC CDR2) of the light chain variable region (VL) of human monoclonal  
 CC antibody LEN. The invention is directed toward mouse-human chimeric  
 CC variants of CC49 Mabs with minimal murine content, to methods of making  
 CC such variants, and to their therapeutic application. Variants are  
 CC provided of huCC49, a humanised Mab formed by grafting hypervariable  
 CC regions from murine CC49 into VL and VH frameworks of human Mabs LEN and  
 CC 21/28. CL, respectively, while retaining murine framework residues  
 CC required for integrity of the antigen combining site structure. HuCC49  
 CC binds to the human pancreaticoma tumor associated glycoprotein-72 (TAG-  
 CC 72), which is found on the surface of certain human tumours. Novel  
 CC variants of huCC49 of the invention have fewer than all 6 CDRs of CC49  
 CC present. Also provided are specifically determining region (SDR) variants  
 CC of huCC49 in which only SDRs of at least 1 CDR from CC49 are present.  
 CC Particular variants of HuCC9 have either L-CDR1 and/or L-CDR2 from human  
 CC Mab LEN. These variants have the same or 2-fold lower affinity constant  
 CC than HuCC49. They are used in claimed methods of treating cancer and for  
 CC detecting cancer cells that express TAG-72  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 38; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WASTRES 7  
 DB 1 WASTRES 7  
 XX  
 RESULT 7  
 AAY32227  
 ID AAY32227 standard; peptide; 7 AA.  
 XX  
 AC AAY32227;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE G-CSF agonist antibody mAb163-93 light chain variable region CDR2.  
 XX  
 KM Granulocyte colony stimulating factor receptor; G-CSF; mouse;  
 KM monoclonal antibody; agonist; screening; neutropenia; therapy;  
 KM complementarity determining region; CDR; mAb163-93.  
 XX  
 OS Mus musculus.  
 XX  
 PN MO955735-A1.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 30-APR-1999; 99WO-US009466.  
 XX  
 PR 30-APR-1998; 98US-0083575P.  
 XX  
 PA (TANO-) TANOX INC.  
 XX  
 PI N1 B, Sun BNC, Sun CRY;  
 XX

DR WPI; 2000-052805/04.  
 XX  
 PT Treatment of neutropenia by stimulating proliferation of neutrophilic  
 PT cell lineage progenitors.  
 XX  
 PS Claim 13; Page 30; 64pp; English.  
 XX  
 CC The present sequence represents complementarity determining region 2  
 CC (CDR2) of the light chain variable region of murine monoclonal antibody  
 CC mAb163-93. This antibody is an example of an agonist molecule that  
 CC specifically binds to or interacts with human granulocyte colony  
 CC stimulating factor (G-CSF) receptor to stimulate cell proliferation and  
 CC differentiation, especially by dimerizing the receptor or activating  
 CC phosphorylation of kinases associated with the receptor. Agonist  
 CC antibodies can be used to stimulate proliferation of G-CSF-dependent  
 CC cells, e.g. to differentiate leading to a repopulation of neutrophilic  
 CC granulocyte lineage cells, especially to treat neutropenia (claimed).  
 CC They can also be used to detect human G-CSF receptor immunologically  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 38; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WASTRES 7  
 DB 1 WASTRES 7  
 XX  
 RESULT 8  
 AAB07952  
 ID AAB07952 standard; peptide; 7 AA.  
 XX  
 AC AAB07952;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE CDR2 sequence from an antibody with affinity for B7 molecules.  
 XX  
 KM Complementarity determining region; CDR; antibody; B7 molecule; B7-1;  
 KM B7-2; humanised immunoglobulin; autoimmune disease; infectious disease;  
 KM inflammatory disorder; systemic lupus erythematosus; diabetes mellitus;  
 KM insulinitis; asthma; arthritis; inflammatory bowel disease; cancer;  
 KM inflammatory dermatitis; multiple sclerosis; transplant rejection;  
 KM proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia;  
 KM thalassemia; aplastic anaemia; myeloid dysplasia syndrome.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200047625-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 09-FEB-2000; 2000WO-US003303.  
 XX  
 PR 12-FEB-1999; 99US-00249011.  
 PR 24-JUN-1999; 99US-00339596.  
 XX  
 PA (GENMY ) GENETICS INST INC.  
 XX  
 PI Co MS, Vasquez M, Carreno B, Ceiniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 DR WPI; 2000-524532/47.  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases.  
 XX  
 PS Disclosure; Page 28; 162pp; English.  
 XX

CC The present sequence represents a complementarily determining region  
 CC (CDR) 2 from the light chains of a murine antibody with having a binding  
 CC specificity to B7-2 molecules. The sequence is used to construct  
 CC humanized immunoglobulins, which comprise an antigen binding region of  
 CC non-human origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), indom errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome

CC Sequence 7 AA:

Query Match 100.0%; Score 38; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
 |||||  
 Db 1 WASTRES 7

# RESULT 9

AAU81257  
 ID AAU81257 standard; peptide; 7 AA.

AC AAU81257;

DT 09-APR-2002 (first entry)

XX Human trkC antibody light chain CDR2 of variable region #2.

XX Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;  
 KW trkA; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;  
 KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;  
 KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;  
 KW nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;  
 KW basopaenia; lymphopaenia; monocytopenia; neutropenia; cancer; ulcer;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;  
 KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;  
 KW cellular degeneration; gene therapy.

XX Homo sapiens.

XX WO200198361-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US020153.

XX 22-JUN-2000; 2000US-0213141P.

XX 05-OCT-2000; 2000US-0238319P.

XX (GETH ) GENENTECH INC.

XX Devaux B, Hongo JS, Presta LG, Shelton DL;

XX WPI, 2002-130790/17.

XX Novel anti-trkC agonist monoclonal antibody useful for treating  
 PT neurodegenerative disease, shows no significant cross-reactivity with  
 PT trkA/trkB, and recognizes epitope in domain 5 of trkC.

XX Claim 13; Fig 11; 121pp; English.

XX The invention relates to an anti-trkC agonist monoclonal antibody which  
 CC shows no significant cross-reactivity with trkA or trkB, and recognizes  
 CC an epitope in domain 5 of trkC. The antibodies of the invention are  
 CC effective in the treatment of cisplatin- or pyridoxine-induced

CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre  
 CC sensory neuropathy, neurodegenerative disease including amyotrophic  
 CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood  
 CC cells such as leukopaenia including eosinopaenia, basopaenia,  
 CC lymphopaenia, monocytopenia, neutropenia, Alzheimer's disease,  
 CC Parkinson's disease, Huntington's disease and tumours. The sequences are  
 CC also useful for inducing angiogenesis for treating wounds, ulcers and  
 CC diabetic complications of sickle cell disease, for treating cardiac  
 CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases  
 CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent  
 CC human and mouse anti-trkC agonist monoclonal antibodies and antibody  
 CC fragments of the invention

CC Sequence 7 AA:

Query Match 100.0%; Score 38; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
 |||||  
 Db 1 WASTRES 7

# RESULT 10

ABP62361  
 ID ABP62361 standard; peptide; 7 AA.

XX ABP62361;

DT 10-OCT-2002 (first entry)

XX Human immunopeptide to HCV E2 glycoprotein light chain CDR #38.

XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
 KW NS3 protein; viral infection.

XX Homo sapiens.

XX WO200259340-A1.

XX 01-AUG-2002.

XX 25-JAN-2002; 2002WO-US002303.

XX 26-JAN-2001; 2001US-0264451P.

XX (SCRI ) SCRIPPS RES INST.

XX Maruyama T, Jones IM, Burton DR, Fox RI;

XX WPI, 2002-599801/64.

XX New human immunopolypeptide with binding specificity for certain envelope  
 PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for  
 PT diagnosing or treating patients having or suspected of having HCV  
 PT infection.

XX Claim 1; Fig 17; 308pp; English.

XX The present invention relates to human immunopolypeptides, produced by a  
 CC phage transfected cell library. The present sequence is one such  
 CC immunopolypeptide. The immunopolypeptides have binding specificity for  
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
 CC cell binding and contains neutralising epitopes, while NS3 is thought to  
 CC be involved in the replication of HCV. The immunopolypeptides are useful  
 CC for diagnosing and treating a patient having or suspected to be having  
 CC HCV infection  
 CC Sequence 7 AA;

Query Match 100.0%; Score 38; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
 |||||  
 DB 1 WASTRES 7

## RESULT 11

AAE29275 ID AAE29275 standard; peptide; 7 AA.

AC AAE29275;

DT 27-JAN-2003 (first entry)

DE Anti-ClfA monoclonal antibody variable light chain CDR2.

XX Clumping factor A; ClfA; fibrinogen; fibrin; ClfA40; ClfA33; N3 protein;  
 KM immunological; staphylococcal infection; impetigo; pneumonia; furuncle;  
 KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy;  
 KM complementarity determining region; CDR.

XX Unidentified.

OS WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.

PR 12-MAR-2001; 2001US-0274611P.

PR 18-JUN-2001; 2001US-0288413P.

PR 30-JUL-2001; 2001US-0308116P.

XX (INH1-) INHIBITEX INC.

PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.

XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for  
 PT treating or preventing Staphylococcus aureus infection e.g. wound  
 PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in  
 PT a human or animal.

XX Claim 30; Page 55; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping  
 CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA  
 CC monoclonal antibody is useful for treating or preventing S. aureus  
 CC infection in a human or animal, and for inhibiting the binding of  
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment  
 CC S. aureus ClfA40 protein, S. aureus ClfA33 protein, or the S. aureus N3  
 CC protein is useful for inducing an immunological response in a human or  
 CC animal. These staphylococcal infections include wound infections, sepsis,  
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The  
 CC present sequence is an anti-ClfA monoclonal antibody variable light chain  
 CC complementarity determining region (CDR)

XX Sequence 7 AA;

QY Query Match 100.0%; Score 38; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
 |||||  
 DB 1 WASTRES 7

RESULT 12  
 ABG68854 ID ABG68854 standard; peptide; 7 AA.

XX ABG68854;

DT 07-OCT-2002 (first entry)

DE CDR2 VL peptide.

XX Cytostatic; virucide; hepatotropic; antiinflammatory; neuroprotective;  
 KM immunosuppressive; antiarthritis; cytokine receptor; interferon; IFN;  
 KM cancer; haematological malignancy; viral infection; hepatitis; human;  
 KM multiple sclerosis; autoimmune disease; arthritis.

XX Synthetic.

XX WO200244197-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-CA001701.

XX 01-DEC-2000; 2000US-00727388.

XX (FISH/) FISH E N.

XX Fish EN;

XX WPI; 2002-547669/58.

XX N-PDSB; ABK97817.

XX Cytokine receptor binding peptide construct, in particular interferon  
 PT receptor binding peptide construct for use as an interferon mimetic,  
 PT comprises a cytokine receptor binding domain incorporated in a molecular  
 PT scaffold.

XX Example 8; Page 50; 105pp; English.

XX This invention relates to a novel cytokine receptor binding peptide  
 CC construct comprising a cytokine receptor binding domain incorporated in a  
 CC suitable molecular scaffold so that the scaffold maintains the binding  
 CC domain in a configuration suitable for binding to the cytokine receptor.

XX The peptides of the invention may have cytostatic, virucide,  
 CC hepatotropic, antiinflammatory, neuroprotective, immunosuppressive and  
 CC antiarthritis activities. A new interferon receptor binding peptide  
 CC construct is useful in the manufacture of a medicament as an interferon  
 CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in  
 CC medical therapies for cancer, haematological malignancies, viral  
 CC infections (hepatitis B or C), multiple sclerosis and autoimmune diseases  
 CC such as arthritis, to detect modulators of IFN action, in screening  
 CC assays to compare the activity and/or interaction with another molecule  
 CC or potential IFN modulator and also in the diagnosis of IFN activity  
 CC related disorders. A nucleic acid encoding the peptide of the invention  
 CC or is useful for the treatment and therapy of the mentioned medical  
 CC conditions. The peptide of the invention has less side effect than those  
 CC of native cytokines. The present sequence represents an interferon  
 CC receptor binding peptide of the invention

XX Sequence 7 AA;

QY Query Match 100.0%; Score 38; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
 |||||  
 DB 1 WASTRES 7

## RESULT 13

AAU70347 ID AAU70347 standard; peptide; 7 AA.

XX AAU70347;  
 AC 14-FEB-2002 (first entry)  
 DT  
 DE Mouse Kappa I light chain CDR2.  
 XX  
 XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
 KW complementarity determining region; framework region; IGBP;  
 KW transgenic plant; immunoglobulin binding protein array; IGM; IGC; IGA;  
 KW Igd; Igs; Igy; Igm; kappa; lambda; CHBP.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO200183806-A1.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-US014349.  
 PF  
 XX 02-MAY-2000; 2000US-00563222.  
 PR  
 XX (EPIC-) EPICYTE PHARM INC.  
 PA  
 XX Hiatt AC, Hein MB;  
 PI  
 XX WPI; 2002-055482/07.  
 DR  
 XX  
 XX Preparing immunoglobulin binding protein array in plant cells by  
 PT transforming the cells with different polynucleotides encoding binding  
 PT protein polypeptides specific to ligand, selecting plant cells for  
 PT preparing array.  
 XX  
 XX Disclosure; Page 14; 129pp; English.  
 PS  
 XX The invention relates to transforming a population of cells (e.g. plant  
 CC cells), comprising using a library of two different polynucleotides  
 CC encoding different immunoglobulin binding protein (IGBP) polypeptides  
 CC that specifically bind to a ligand or form one or more disulphide bonds  
 CC with polypeptides in transfected cells, to generate an IGBP that binds to  
 CC a ligand, and transformed plant cells are selected, and preparing an IGBP  
 CC array in plant cells. At least one peptide sequence has at least 75%  
 CC sequence identity to a framework region (FR) of a native Igm, Igc, Iga,  
 CC Igd, Ige, Igy, kappa or lambda immunoglobulin molecule. The method is  
 CC useful for preparing an immunoglobulin binding protein array, preferably  
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
 CC discovery of e.g. screening assays of IGBPs having desired  
 CC characteristics. The present sequence is a mammalian immunoglobulin  
 CC derived peptide that may be incorporated into an IGBP of the invention  
 CC  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 100.0%; Score 38; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;  
 QY 1 WASTRES 7  
 DB 1 WASTRES 7  
 XX  
 XX RESULT 14  
 ID AAU70335 standard; peptide; 7 AA.  
 XX  
 XX AAU70335;  
 AC  
 XX 14-FEB-2002 (first entry)  
 DT  
 XX Human Kappa IV light chain CDR2.  
 DE  
 XX

KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
 KW complementarity determining region; framework region; IGBP;  
 KW transgenic plant; immunoglobulin binding protein array; IGM; IGC; IGA;  
 KW Igd; Igs; Igy; Igm; kappa; lambda; CHBP.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200183806-A1.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-US014349.  
 PF  
 XX 02-MAY-2000; 2000US-00563222.  
 PR  
 XX (EPIC-) EPICYTE PHARM INC.  
 PA  
 XX Hiatt AC, Hein MB;  
 PI  
 XX WPI; 2002-055482/07.  
 DR  
 XX  
 XX Preparing immunoglobulin binding protein array in plant cells by  
 PT transforming the cells with different polynucleotides encoding binding  
 PT protein polypeptides specific to ligand, selecting plant cells for  
 PT preparing array.  
 XX  
 XX Disclosure; Page 14; 129pp; English.  
 PS  
 XX The invention relates to transforming a population of cells (e.g. plant  
 CC cells), comprising using a library of two different polynucleotides  
 CC encoding different immunoglobulin binding protein (IGBP) polypeptides  
 CC that specifically bind to a ligand or form one or more disulphide bonds  
 CC with polypeptides in transfected cells, to generate an IGBP that binds to  
 CC a ligand, and transformed plant cells are selected, and preparing an IGBP  
 CC array in plant cells. At least one peptide sequence has at least 75%  
 CC sequence identity to a framework region (FR) of a native Igm, Igc, Iga,  
 CC Igd, Ige, Igy, kappa or lambda immunoglobulin molecule. The method is  
 CC useful for preparing an immunoglobulin binding protein array, preferably  
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
 CC discovery of e.g. screening assays of IGBPs having desired  
 CC characteristics. The present sequence is a mammalian immunoglobulin  
 CC derived peptide that may be incorporated into an IGBP of the invention  
 CC  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 100.0%; Score 38; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;  
 QY 1 WASTRES 7  
 DB 1 WASTRES 7  
 XX  
 XX RESULT 15  
 ID AAE34369 standard; peptide; 7 AA.  
 XX  
 XX AAE34369;  
 AC  
 XX 14-MAY-2003 (first entry)  
 DT  
 XX Escherichia coli light chain variable region CDR2.  
 DE  
 XX S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;  
 KW hepatotropic; complementarity determining region; CDR.  
 KW Escherichia coli.  
 OS  
 XX WO200292819-A1.  
 PN  
 XX

```

PD 21-NOV-2002.
XX
XX 15-MAY-2002; 2002MO-KR000905.
XX
XX 16-MAY-2001; 2001KR-00026634.
XX
XX (YUHA-) YUHAN CORP.
XX
XX Lee JW, Ko IY, Kang HK, Song MY, Song TH, Kim CS;
XX WPI; 2003-140281/13.
XX
XX New light and heavy chain variable regions of a monoclonal antibody
XX against the S-surface antigen of the hepatitis B virus (HBV), useful for
XX neutralizing or removing HBV, or for preventing or treating HBV
XX infection.
XX
XX Claim 11; Page 17; 20pp; English.
XX
XX The invention relates to light and heavy chain variable regions of a
XX monoclonal antibody against S-surface antigen of the hepatitis B virus
XX (HBV). The variable regions of the antibodies are useful against HBV S-
XX surface antigens, e.g., adr, adw, ayr or ayw, particularly for
XX neutralizing or removing HBV. They may also be employed to treat or
XX prevent HBV infection. The present sequence is Escherichia coli light
XX chain variable region complementarity determining region (CDR)
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 38; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7
   |||||
Db 1 WASTRES 7

Search completed: March 1, 2005, 17:36:08
Job time : 53.3385 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 13.6769 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-19

Perfect score: 38

Sequence: 1 WASTRES 7

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	1	US-08-360-125-20 Sequence 20, Appl
2	38	100.0	7	2	US-08-450-578-20 Sequence 20, Appl
3	38	100.0	7	2	US-09-017-628-20 Sequence 20, Appl
4	38	100.0	7	2	US-09-014-880-20 Sequence 20, Appl
5	38	100.0	7	3	US-07-987-264-5 Sequence 5, Appl
6	38	100.0	7	4	US-08-450-363-20 Sequence 20, Appl
7	38	100.0	7	4	US-09-563-222C-15 Sequence 15, Appl
8	38	100.0	7	4	US-09-563-222C-27 Sequence 27, Appl
9	38	100.0	7	4	US-09-467-903-20 Sequence 20, Appl
10	38	100.0	7	4	US-09-830-748B-8 Sequence 8, Appl
11	38	100.0	7	4	US-09-627-896B-18 Sequence 18, Appl
12	38	100.0	7	5	PCT-US93-08435-24 Sequence 24, Appl
13	38	100.0	7	5	PCT-US93-08435-37 Sequence 37, Appl
14	38	100.0	7	5	PCT-US93-08435-41 Sequence 41, Appl
15	38	100.0	101	4	US-08-627-896B-28 Sequence 28, Appl
16	38	100.0	109	2	US-08-308-494A-23 Sequence 23, Appl
17	38	100.0	110	3	US-08-957-001B-5 Sequence 5, Appl
18	38	100.0	110	3	US-08-957-001B-24 Sequence 24, Appl
19	38	100.0	110	3	US-09-496-301-5 Sequence 5, Appl
20	38	100.0	110	3	US-09-496-301-24 Sequence 24, Appl
21	38	100.0	112	1	US-07-942-245-30 Sequence 30, Appl
22	38	100.0	112	2	US-07-916-098A-15 Sequence 15, Appl
23	38	100.0	112	4	US-08-435-516-4 Sequence 4, Appl
24	38	100.0	112	4	US-08-435-516-28 Sequence 28, Appl
25	38	100.0	113	1	US-08-690-102A-2 Sequence 2, Appl
26	38	100.0	113	1	US-08-690-102A-6 Sequence 6, Appl
27	38	100.0	113	3	US-08-483-749A-16 Sequence 16, Appl

28	38	100.0	113	3	US-09-127-902-2 Sequence 2, Appl
29	38	100.0	113	3	US-09-127-902-6 Sequence 6, Appl
30	38	100.0	113	3	US-09-155-107-2 Sequence 2, Appl
31	38	100.0	113	3	US-09-155-107-6 Sequence 6, Appl
32	38	100.0	113	3	US-09-155-107-20 Sequence 20, Appl
33	38	100.0	113	3	US-08-525-539A-80 Sequence 80, Appl
34	38	100.0	113	4	US-09-301-593-2 Sequence 2, Appl
35	38	100.0	113	4	US-09-301-593-4 Sequence 4, Appl
36	38	100.0	113	4	US-09-301-593-6 Sequence 6, Appl
37	38	100.0	113	4	US-09-301-593-32 Sequence 32, Appl
38	38	100.0	113	4	US-09-301-593-33 Sequence 33, Appl
39	38	100.0	113	4	US-09-301-593-34 Sequence 34, Appl
40	38	100.0	113	4	US-09-274-163E-16 Sequence 16, Appl
41	38	100.0	113	5	PCT-US93-08435-4 Sequence 4, Appl
42	38	100.0	113	5	PCT-US93-08435-6 Sequence 6, Appl
43	38	100.0	113	5	PCT-US93-08435-8 Sequence 8, Appl
44	38	100.0	113	5	PCT-US93-11611-5 Sequence 5, Appl
45	38	100.0	113	5	PCT-US95-09641-2 Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-360-125-20  
; Sequence 20, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saito HOSOKAWA  
; APPLICANT: Toshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5767246hiko ITO  
; APPLICANT: Kazuhiro NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; TITLE OF INVENTION: Cell Membrane  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Wenderoth, Lind & Penack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-20

Query Match 100.0%; Score 38; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 2  
US-08-450-578-20  
Sequence 20, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: SAIKO HOSOKAWA  
APPLICANT: TOSHIKAKI TAGAWA  
APPLICANT: YOKO HIRAKAWA  
APPLICANT: NO. 5837845HIKO ITO  
APPLICANT: KAZUHIRO NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. ChaeK, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-20

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7



RESULT 3  
US-09-017-628-20  
Sequence 20, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Tohshiki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287iniko  
APPLICANT: NAGAIKE, Kazuhiko  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-20

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 4  
US-09-014-880-20  
Sequence 20, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human antibody GAH  
US-09-014-880-20

Query Match 100.0%; Score 38; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 5  
US-07-987-264-5  
Sequence 5, Application US/07987264  
Patent No. 6204366  
GENERAL INFORMATION:  
APPLICANT: VERHOEVEN, MARTINE ELISA  
TITLE OF INVENTION: SPECIFIC BINDING AGENTS  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/987,264  
FILING DATE: 08-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9019553.8  
FILING DATE: 07-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB PCT/GB91/01511  
FILING DATE: 05-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 200232/P3095USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-987-264-5

Query Match 100.0%; Score 38; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7

## RESULT 6

US-08-450-363-20  
Sequence 20, Application US/08450363  
Patent No. 6436434  
GENERAL INFORMATION:  
APPLICANT: SAIKO HOSOKAWA  
APPLICANT: TOSHIAKI TAGAWA  
APPLICANT: YOKO HIRAKAWA  
APPLICANT: NO. 6436434/1HIKO ITO  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 142  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
CLASSIFICATION: 530  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody GAH  
ORGANELLE:

IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-363-20  
Query Match 100.0%; Score 38; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7

## RESULT 7

US-09-563-222C-15  
Sequence 15, Application US/09563222C  
Patent No. 6696620  
GENERAL INFORMATION:  
APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
APPLICANT: HIATT, ANDREW C.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
FILE REFERENCE: 068904-0501  
CURRENT APPLICATION NUMBER: US/09/563,222C  
CURRENT FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: PCT/US01/14349  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/563,222  
PRIOR FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-563-222C-15

Query Match 100.0%; Score 38; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7

## RESULT 8

US-09-563-222C-27  
Sequence 27, Application US/09563222C  
Patent No. 6696620  
GENERAL INFORMATION:

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; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-563-222C-27

Query Match          100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7
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Db 1 WASTRES 7

RESULT 9
US-09-467-903-20
; Sequence 20, Application US/09467903
; Patent No. 6787153
; GENERAL INFORMATION:
; APPLICANT: SAIKO HOSOKAWA
;              TOSHIKAZU TAGAWA
;              YOKO HIRAKAWA
;              NO. 6787153HIKO ITO
;              KAZUHIRO NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
;                      Specifically Binding to Surface Antigen of Cancer
;                      Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,903
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,363
; FILING DATE: May 25, 1995
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER: JP158859/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JP158860/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JP158861/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JP158861/1991
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.

; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: <Unknown>
; TELE: <Unknown>
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: <Unknown>
; ANTI-SENSE: <Unknown>
; ORIGINAL SOURCE:
; ORGANISM: <Unknown>
; STRAIN: <Unknown>
; INDIVIDUAL ISOLATE: <Unknown>
; DEVELOPMENTAL STAGE: <Unknown>
; HAPLOTYPE: <Unknown>
; TISSUE TYPE: <Unknown>
; CELL TYPE: Hybridoma producing human antibody G4H
; CELL LINE: <Unknown>
; ORGANELLE: <Unknown>
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: <Unknown>
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: <Unknown>
; MAP POSITION: <Unknown>
; UNITS: <Unknown>
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
; US-09-467-903-20

Query Match          100.0%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WASTRES 7
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Db 1 WASTRES 7

RESULT 10
US-09-830-748B-8
; Sequence 8, Application US/09830748B
; Patent No. 6818749
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by The
;              Secretary of the Department of Health and Human Services
; APPLICANT: Kashimiri, Syed V.S.
; APPLICANT: Padian, Eduardo A.
; APPLICANT: Jeffery, Schlom
; TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49
; FILE REFERENCE: 4239-61725
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;; CURRENT APPLICATION NUMBER: US/09/830,748B  
;; CURRENT FILING DATE: 2001-04-30  
;; PRIOR APPLICATION NUMBER: PCT/ US99/25552  
;; PRIOR FILING DATE: 1999-10-29  
;; PRIOR APPLICATION NUMBER: US 60/106,757  
;; PRIOR FILING DATE: 1998-11-02  
;; PRIOR APPLICATION NUMBER: US 60/106,534  
;; PRIOR FILING DATE: 1998-10-31  
;; NUMBER OF SEQ ID NOS: 44  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO: 8  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-830-748B-8

Query Match 100.0%; Score 38; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 11  
US-09-627-896B-18  
;; Sequence 18; Application US/09627896B  
;; Patent No. 6827934  
;; GENERAL INFORMATION:  
;; APPLICANT: CO, MAN SUNG  
;; APPLICANT: VASQUEZ, MAXIMILIANO  
;; APPLICANT: CARRENO, BEATRIZ  
;; APPLICANT: CELNIKER, ABBIE CHERYL  
;; APPLICANT: COLLINS, MARY  
;; APPLICANT: GOLDMAN, SAMUEL  
;; APPLICANT: GRAY, GARY S.  
;; APPLICANT: KNIGHT, ANDREA  
;; APPLICANT: O'HARA, DENISE  
;; APPLICANT: RUP, BONITA  
;; APPLICANT: VEIDMAN, GEERTRUDA M.  
;; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
;; FILE REFERENCE: 08702.0081-01000  
;; CURRENT APPLICATION NUMBER: US/09/627,896B  
;; CURRENT FILING DATE: 2000-07-27  
;; NUMBER OF SEQ ID NOS: 32  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO: 18  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized  
;; OTHER INFORMATION: murine anti-human B7-2 light chain  
US-09-627-896B-18

Query Match 100.0%; Score 38; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 12  
PCT-US93-08435-24  
;; Sequence 24; Application PC/TUS9308435  
;; GENERAL INFORMATION:  
;; APPLICANT: SmithKline Beecham, Corporation  
;; APPLICANT: U. S. Government, Secretary of  
;; APPLICANT: the Navy

;; APPLICANT: U. S. Government, Secretary of  
;; APPLICANT: the Army  
;; TITLE OF INVENTION: Novel Antibodies for Confering Passive  
;; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man  
;; NUMBER OF SEQUENCES: 61  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Howson and Howson  
;; STREET: Box 457, 321 Norristown Road  
;; CITY: Spring House  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19477  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US93/08435  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/941,654  
;; FILING DATE: 09-SEP-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bak, Mary E.  
;; REGISTRATION NUMBER: 31,215  
;; REFERENCE/DOCKET NUMBER: SBC P50107  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 540-9200  
;; TELEFAX: (215) 540-5818  
;; INFORMATION FOR SEQ ID NO: 24:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
PCT-US93-08435-24

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 13  
PCT-US93-08435-37  
;; Sequence 37; Application PC/TUS9308435  
;; GENERAL INFORMATION:  
;; APPLICANT: SmithKline Beecham, Corporation  
;; APPLICANT: U. S. Government, Secretary of  
;; APPLICANT: the Navy  
;; APPLICANT: U. S. Government, Secretary of  
;; APPLICANT: the Army  
;; TITLE OF INVENTION: Novel Antibodies for Confering Passive  
;; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man  
;; NUMBER OF SEQUENCES: 61  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Howson and Howson  
;; STREET: Box 457, 321 Norristown Road  
;; CITY: Spring House  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19477  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/941,654  
FILING DATE: 09-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: SBC P50107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9200  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
PCT-US93-08435-37

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 14  
PCT-US93-08435-41  
Sequence 41, Application PC/TUS9308435  
GENERAL INFORMATION:  
APPLICANT: SmithKline Beecham, Corporation  
APPLICANT: U. S. Government, Secretary of  
APPLICANT: the Navy  
APPLICANT: U. S. Government, Secretary of  
TITLE OF INVENTION: Novel Antibodies for Confering Passive  
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 Norrisdown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/941,654  
FILING DATE: 09-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: SBC P50107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9200  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown

MOLECULE TYPE: protein  
PCT-US93-08435-41

Query Match 100.0%; Score 38; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 15  
US-09-627-896B-28  
Sequence 28, Application US/09627896B  
Patent No. 6827934  
GENERAL INFORMATION:  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
APPLICANT: CARRENO, BEATRIZ  
APPLICANT: CELINKER, ABBIE CHERYL  
APPLICANT: COLLINS, MARY  
APPLICANT: GOLDMAN, SAMUEL  
APPLICANT: GRAY, GARY S.  
APPLICANT: KNIGHT, ANDREA  
APPLICANT: O'HARA, DENISE  
APPLICANT: RUP, BONITA  
APPLICANT: VELDMAN, GEBTRUIDA M.  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
TITLE OF INVENTION: OF TREATMENT THEREWITH  
FILE REFERENCE: 08702, 0081-01000  
CURRENT APPLICATION NUMBER: US/09/627, 896B  
CURRENT FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 28  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: HZF light chain variable region  
US-09-627-896B-28

Query Match 100.0%; Score 38; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
Db 56 WASTRES 62

Search completed: March 1, 2005, 17:46:57  
Job time : 13.6769 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 37.4766 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-19

Perfect score: 38

Sequence: 1 WASTRES 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	7	9	US-09-749-831-5
2	38	100.0	7	9	US-09-828-708-42
3	38	100.0	7	9	US-09-828-708-46
4	38	100.0	7	9	US-09-249-011A-18
5	38	100.0	7	10	US-09-563-222-15
6	38	100.0	7	10	US-09-563-222-15
7	38	100.0	7	13	US-10-146-305-10
8	38	100.0	7	14	US-10-071-962-19
9	38	100.0	7	16	US-10-312-316-29
10	38	100.0	7	16	US-10-469-125-5
11	38	100.0	7	16	US-10-783-950-15
12	38	100.0	7	16	US-10-783-950-27
13	38	100.0	7	17	US-10-483-994-5

14	38	100.0	7	17	US-10-483-993-5	Sequence 5, Appli
15	38	100.0	82	14	US-10-078-958-15	Sequence 15, Appl
16	38	100.0	94	9	US-09-905-243-60	Sequence 89, Appl
17	38	100.0	101	14	US-10-194-975-89	Sequence 25, Appl
18	38	100.0	101	14	US-10-125-687-25	Sequence 36, Appl
19	38	100.0	101	15	US-10-308-817-36	Sequence 103, App
20	38	100.0	101	15	US-10-453-698-36	Sequence 142, App
21	38	100.0	101	16	US-10-379-992-103	Sequence 148, App
22	38	100.0	105	14	US-10-010-729-37	Sequence 149, App
23	38	100.0	107	14	US-10-325-694-142	Sequence 152, App
24	38	100.0	107	14	US-10-325-694-148	Sequence 1, Appli
25	38	100.0	107	14	US-10-325-694-148	Sequence 4, Appli
26	38	100.0	107	14	US-10-325-694-148	Sequence 6, Appli
27	38	100.0	109	9	US-09-828-708-4	Sequence 32, Appl
28	38	100.0	109	9	US-09-828-708-4	Sequence 34, Appl
29	38	100.0	112	14	US-10-056-052-6	Sequence 3, Appl
30	38	100.0	112	14	US-10-056-052-10	Sequence 10, Appl
31	38	100.0	112	14	US-10-056-052-10	Sequence 14, Appl
32	38	100.0	112	14	US-10-056-052-18	Sequence 18, Appl
33	38	100.0	112	14	US-10-229-335-4	Sequence 4, Appli
34	38	100.0	112	14	US-10-229-335-28	Sequence 28, Appl
35	38	100.0	113	9	US-09-301-593-2	Sequence 2, Appli
36	38	100.0	113	9	US-09-301-593-4	Sequence 4, Appli
37	38	100.0	113	9	US-09-301-593-6	Sequence 6, Appli
38	38	100.0	113	9	US-09-301-593-12	Sequence 32, Appl
39	38	100.0	113	9	US-09-301-593-13	Sequence 33, Appl
40	38	100.0	113	9	US-09-301-593-34	Sequence 34, Appl
41	38	100.0	113	9	US-09-741-843-2	Sequence 6, Appli
42	38	100.0	113	9	US-09-741-843-6	Sequence 16, Appl
43	38	100.0	113	9	US-09-274-163E-16	Sequence 80, Appl
44	38	100.0	113	9	US-09-956-206A-80	Sequence 2, Appli
45	38	100.0	113	10	US-09-894-839-2	

## ALIGNMENTS

RESULT 1  
US-09-749-831-5  
; Sequence 5, Application US/09749831  
; Publication No. US20020086978A1  
; GENERAL INFORMATION:  
; APPLICANT: VERHOEVEN, MARTINE ELISA  
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Winthrop LLP  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/749, 831  
; FILING DATE: 04-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/987, 264  
; FILING DATE: 08-MAR-1993  
; APPLICATION NUMBER: GB PCT/GB91/01511  
; FILING DATE: 05-SEP-1991  
; APPLICATION NUMBER: GB 9019553.8  
; FILING DATE: 07-SEP-1990  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 5  
US-09-749-831-5

Query Match 100.0%; Score 38; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 2  
US-09-828-708-43  
Sequence 43, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.  
APPLICANT: Burton, D.  
APPLICANT: Schaller, M.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 43  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-43

Query Match 100.0%; Score 38; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 3  
US-09-828-708-46  
Sequence 46, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.  
APPLICANT: Burton, D.  
APPLICANT: Schaller, M.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 46  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-46

Query Match 100.0%; Score 38; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 4  
US-09-249-011A-18  
Sequence 18, Application US/09249011A  
Patent No. US20020176855A1  
GENERAL INFORMATION:  
APPLICANT: CO. MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
APPLICANT: CARENNO, BEATRIZ  
APPLICANT: CELINKER, ABIE CHERYL  
APPLICANT: COLLINS, MARY  
APPLICANT: GOLDMAN, SAMUEL  
APPLICANT: GRAY, GARY S.  
APPLICANT: KNIGHT, ANDREA  
APPLICANT: O'HARA, DENISE  
APPLICANT: RUP, BONITA  
APPLICANT: WELDMAN, GERTTRUDA M.

TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
FILE REFERENCE: 08702.0081-00000  
CURRENT APPLICATION NUMBER: US/09/249,011A  
CURRENT FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 18  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized  
US-09-249-011A-18

Query Match 100.0%; Score 38; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 5  
US-09-563-222-15  
Sequence 15, Application US/09563222  
Publication No. US20030079253A1  
GENERAL INFORMATION:  
APPLICANT: Hlatc, Andrew  
APPLICANT: Hlatc, Mich B.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
FILE REFERENCE: 310098.406  
CURRENT APPLICATION NUMBER: US/09/563,222  
CURRENT FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-563-222-15

Query Match 100.0%; Score 38; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 1 WASTRES 7

RESULT 6  
US-09-563-222-27



```
; Sequence 27, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hielt, Andrew
; APPLICANT: Hehn, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-27

Query Match
Best Local Similarity 100.0%; Score 38; DB 10; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 7
US-10-146-305-10
; Sequence 10, Application US/10146305
; Publication No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; FILE REFERENCE: OVI7440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Kopatentia 1.71
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-10

Query Match
Best Local Similarity 100.0%; Score 38; DB 13; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 8
US-10-071-962-19
; Sequence 19, Application US/10071962
; Publication No. US20030170237A1
; GENERAL INFORMATION:
; APPLICANT: Bauli N.
; APPLICANT: Bill N.C. Sun
; APPLICANT: Cedilly R.Y. Sun
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and
; FILE REFERENCE: 98-3
; CURRENT APPLICATION NUMBER: US/10/071,962
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/303,155A
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,575
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; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-10-071-962-19

Query Match
Best Local Similarity 100.0%; Score 38; DB 14; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 9
US-10-312-316-29
; Sequence 29, Application US/10312316
; Publication No. US20040137513A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Hongo, Jo-Anne S.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
; FILE REFERENCE: GENENT 0400PC
; CURRENT APPLICATION NUMBER: US/10/312,316
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/238,319
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-316-29

Query Match
Best Local Similarity 100.0%; Score 38; DB 16; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7
Db 1 WASTRES 7

RESULT 10
US-10-469-125-5
; Sequence 5, Application US/10469125
; Publication No. US20040143101A1
; GENERAL INFORMATION:
; APPLICANT: Solcis, Daniel A.
; APPLICANT: Burch, Ronald M.
; APPLICANT: Shukla, Rajiv
; TITLE OF INVENTION: IMMUNOGLOBULIN CONSTRUCT CONTAINING ANTI-MUCIN VARIABLE DOMAIN SE
; FILE REFERENCE: 02755/100G273-US1
; CURRENT APPLICATION NUMBER: US/10/469,125
; CURRENT FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: US 60/281,182
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/US02/10304
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-469-125-5

Query Match  
Best Local Similarity 100.0%; Score 38; DB 16; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7

RESULT 11  
US-10-783-950-15

; Sequence 15, Application US/10783950  
; Publication No. US20040199945A1  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/10/783,950  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-783-950-15

Query Match  
Best Local Similarity 100.0%; Score 38; DB 16; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7

RESULT 12  
US-10-783-950-27

; Sequence 27, Application US/10783950  
; Publication No. US20040199945A1  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/10/783,950  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-783-950-27

Query Match  
Best Local Similarity 100.0%; Score 38; DB 16; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7

RESULT 13  
US-10-483-994-5

; Sequence 5, Application US/10483994  
; Publication No. US20050032132A1  
; GENERAL INFORMATION:  
; APPLICANT: MITSUBISHI PHARMA CORPORATION  
; TITLE OF INVENTION: CANCER DIAGNOSTICS  
; FILE REFERENCE: 02030W00  
; CURRENT APPLICATION NUMBER: US/10/483,994  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: JP P2001-224054  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-483-994-5

Query Match  
Best Local Similarity 100.0%; Score 38; DB 17; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7

RESULT 14  
US-10-483-993-5

; Sequence 5, Application US/10483993  
; Publication No. US20050037061A1  
; GENERAL INFORMATION:  
; APPLICANT: MITSUBISHI PHARMA CORPORATION  
; TITLE OF INVENTION: REMEDIES FOR MAMMARY CANCER  
; FILE REFERENCE: 02031W00  
; CURRENT APPLICATION NUMBER: US/10/483,993  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: JP P2001-224596  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-483-993-5

Query Match  
Best Local Similarity 100.0%; Score 38; DB 17; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
1 WASTRES 7

RESULT 15  
US-10-078-958-15

; Sequence 15, Application US/10078958  
; Publication No. US20030070185A1  
; GENERAL INFORMATION:  
; APPLICANT: JAKOBOVITS, AYA  
; APPLICANT: KUCHERLAPATI, RAJU  
; APPLICANT: KLAPHOLZ, SUSAN

APPLICANT: MENDEZ, MICHAEL J.  
APPLICANT: GREEN, LARRY  
TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOC1 INCLUDING  
TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED  
TITLE OF INVENTION: THEREFROM  
FILE REFERENCE: CELL 4.18 CON  
CURRENT APPLICATION NUMBER: US/10/078,958  
CURRENT FILING DATE: 2002-02-19  
PRIOR APPLICATION NUMBER: 08/759,620  
PRIOR FILING DATE: 1996-12-03  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 82  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-078-958-15

Query Match 100.0%; Score 38; DB 14; Length 82;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
Db 37 WASTRES 43

Search completed: March 1, 2005, 17:52:51  
Job time : 37.4769 secs

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## OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 9.47692 Seconds  
(without alignments)  
71.069 Million cell updates/sec

Title: US-10-071-962-19

Perfect score: 38

Sequence: 1 WASTRES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir79: \*  
2: pir1: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	81	2 PH1048	Ig light chain V r
2	38	100.0	92	2 S37532	Ig kappa chain V r
3	38	100.0	92	2 S37533	Ig kappa chain V r
4	38	100.0	92	2 S37530	Ig kappa chain V r
5	38	100.0	92	2 S37535	Ig kappa chain V r
6	38	100.0	92	2 S37531	Ig kappa chain V r
7	38	100.0	92	2 S37534	Ig kappa chain V r
8	38	100.0	92	2 S37529	Ig kappa chain V r
9	38	100.0	98	2 S19974	Ig kappa chain V r
10	38	100.0	101	2 PH0869	Ig kappa chain V r
11	38	100.0	101	2 PH1046	Ig light chain V r
12	38	100.0	101	2 S26337	Ig light chain V r
13	38	100.0	102	2 A34153	Ig kappa chain V-I
14	38	100.0	103	2 PH1047	Ig light chain V r
15	38	100.0	103	2 PH1051	Ig light chain V r
16	38	100.0	103	2 PH1052	Ig light chain V r
17	38	100.0	103	2 PH1050	Ig light chain V r
18	38	100.0	103	2 PH1054	Ig light chain V r
19	38	100.0	104	2 PH1101	Ig light chain V r
20	38	100.0	104	2 F38601	Ig kappa chain V r
21	38	100.0	104	2 PH1102	Ig light chain V r
22	38	100.0	104	2 PH1103	Ig light chain V r
23	38	100.0	104	2 PH1104	Ig light chain V r
24	38	100.0	106	2 A49138	Ig kappa chain V r
25	38	100.0	111	2 S03304	Ig kappa chain V r
26	38	100.0	111	2 G30502	Ig kappa chain V r
27	38	100.0	112	2 S09970	Ig kappa chain V-J
28	38	100.0	112	2 PL0265	Ig kappa chain V r
29	38	100.0	112	2 S43103	Ig kappa chain V-J

30	38	100.0	113	2 S34002	Ig kappa chain V r
31	38	100.0	113	2 S34003	Ig kappa chain V r
32	38	100.0	113	2 S30523	Ig kappa chain V r
33	38	100.0	113	2 PL0263	Ig kappa chain V r
34	38	100.0	114	1 K4HUN	Ig kappa chain V-I
35	38	100.0	114	2 S44119	Ig kappa chain V-J
36	38	100.0	114	2 S44116	Ig kappa chain V-J
37	38	100.0	118	2 PR0356	Ig kappa chain V r
38	38	100.0	120	2 S51147	antibody light cha
39	38	100.0	120	2 G33932	Ig kappa chain pre
40	38	100.0	121	1 K4HU	Ig kappa chain pre
41	38	100.0	129	2 S40329	Ig kappa chain V-J
42	38	100.0	129	2 S40347	Ig kappa chain - h
43	38	100.0	133	1 K4HUI	Ig kappa chain pre
44	38	100.0	133	2 PS0023	Ig kappa chain pre
45	38	100.0	134	2 S49531	anti-Sm antibody V

## ALIGNMENTS

## RESULT 1

PH1048  
Ig light chain V region (clone 165.49) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996

C:Accession: PH1048

R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1048

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-81 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

## Query Match

Best Local Similarity 100.0%; Score 38; DB 2; Length 81;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Query

1 WASTRES 7

35 WASTRES 41

## RESULT 2

S37532  
Ig kappa chain V region (V-kappa 4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S37532

R:Klein, U.; Kuipers, R.; Rajewsky, K.

Submitted to the EMBL Data Library, September 1993

A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37532

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-References: EMBL:Z26628; NID:9405706; PTDN:CA81381.1; PTD:9405707

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 100.0%; Score 38; DB 2; Length 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Query

1 WASTRES 7

34 WASTRES 40

RESULT 3  
S37533  
Ig kappa chain V region (V-kappa 4) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S37533  
R:Klein, U.; Kuipers, R.; Rajewsky, K.  
submitted to the EMBL Data Library, September 1993  
A/Description: Human Igm(+) IgD(+) cells, the major B cell subset in the peripheral blood  
A/Reference number: S37501  
A/Accession: S37533  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-92 <KLE>  
A/Cross-references: EMBL:Z26629; NID:G405708; PIDN:CAA81380.1; PID:G405709  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 34 WASTRES 40

RESULT 4  
S37530  
Ig kappa chain V region (V-kappa 4) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S37530  
R:Klein, U.; Kuipers, R.; Rajewsky, K.  
submitted to the EMBL Data Library, September 1993  
A/Description: Human Igm(+) IgD(+) cells, the major B cell subset in the peripheral blood  
A/Reference number: S37501  
A/Accession: S37530  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-92 <KLE>  
A/Cross-references: EMBL:Z26630; NID:G405702; PIDN:CAA81383.1; PID:G405703  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 34 WASTRES 40

RESULT 5  
S37535  
Ig kappa chain V region (V-kappa 4) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S37535  
R:Klein, U.; Kuipers, R.; Rajewsky, K.  
submitted to the EMBL Data Library, September 1993  
A/Description: Human Igm(+) IgD(+) cells, the major B cell subset in the peripheral blood  
A/Reference number: S37501  
A/Accession: S37535  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-92 <KLE>  
A/Cross-references: EMBL:Z26625; NID:G405712; PIDN:CAA81378.1; PID:G405713  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 34 WASTRES 40

RESULT 6  
S37531  
Ig kappa chain V region (V-kappa 4) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S37531  
R:Klein, U.; Kuipers, R.; Rajewsky, K.  
submitted to the EMBL Data Library, September 1993  
A/Description: Human Igm(+) IgD(+) cells, the major B cell subset in the peripheral blood  
A/Reference number: S37501  
A/Accession: S37531  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-92 <KLE>  
A/Cross-references: EMBL:Z26629; NID:G405704; PIDN:CAA81382.1; PID:G405705  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 34 WASTRES 40

RESULT 7  
S37534  
Ig kappa chain V region (V-kappa 4) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S37534  
R:Klein, U.; Kuipers, R.; Rajewsky, K.  
submitted to the EMBL Data Library, September 1993  
A/Description: Human Igm(+) IgD(+) cells, the major B cell subset in the peripheral blood  
A/Reference number: S37501  
A/Accession: S37534  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-92 <KLE>  
A/Cross-references: EMBL:Z26626; NID:G405710; PIDN:CAA81379.1; PID:G405711  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||||  
Db 34 WASTRES 40

RESULT 8  
S37529  
Ig kappa chain V region (V-kappa 4) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S37529  
R:Klein, U.; Kuipers, R.; Rajewsky, K.  
submitted to the EMBL Data Library, September 1993  
A/Description: Human Igm(+) IgD(+) cells, the major B cell subset in the peripheral blood,

A:Reference number: S37501  
 A:Accession: S37529  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-92 <TIL>  
 A:Cross-references: EMBL:Z26631; NID:G405700; PIDN:CAA81384.1; PID:G405701  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 38; DB 2; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 0.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 |||||  
 Db 34 WASTRES 40

## RESULT 9

S19974  
 Ig kappa chain V region (M-T406) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S19974  
 R:Weissenborn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.  
 submitted to the EMBL Data Library, March 1992  
 A:Description: Structural characterization of CD4 mAb.  
 A:Reference number: S19963  
 A:Accession: S19974  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-98 <WEI>  
 A:Cross-references: EMBL:X65096; NID:G52294; PIDN:CAA46224.1; PID:G52295  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-80/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 0.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 |||||  
 Db 40 WASTRES 46

## RESULT 10

PH0869  
 Ig kappa chain V region (anti-DNA, H2F) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jan-2000  
 C:Accession: PH0869  
 R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.  
 J. Exp. Med. 174, 1639-1652, 1991  
 A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype  
 A:Reference number: PH0862; MUID:92078875; PMID:1660528  
 A:Accession: PH0869  
 A:Molecule type: DNA  
 A:Residues: 1-101 <MAN>  
 A:Note: residues 28-33 were obtained from Figure 4  
 C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-23/Region: framework 1  
 F:16-96/Domain: immunoglobulin homology <IMM>  
 F:24-40/Region: complementarity-determining 1  
 F:41-55/Region: framework 2  
 F:56-62/Region: complementarity-determining 2  
 F:63-94/Region: framework 3  
 F:95-101/Region: complementarity-determining 3

Query Match 100.0%; Score 38; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 WASTRES 7  
 |||||  
 Db 56 WASTRES 62

## RESULT 11

PH1046  
 Ig light chain V region (clone 202.9) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
 C:Accession: PH1046  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
 A:Reference number: PH0971; MUID:92381444; PMID:1512540  
 A:Accession: PH1046  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <TIL>  
 A:Experimental source: B cell, strain [NZB x NZW] F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 0.44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 |||||  
 Db 56 WASTRES 62

## RESULT 12

S26337  
 Ig light chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Mar-1998 #sequence\_revision 19-Mar-1998 #text\_change 20-Jun-2000  
 C:Accession: S26337; S78449  
 R:Stark, S.B.; Caton, A.J.  
 J. Exp. Med. 174, 613-624, 1991  
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e  
 A:Reference number: S26309; MUID:91341421; PMID:1908510  
 A:Accession: S26337  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <STA>  
 A:Cross-references: EMBL:X59193  
 R:Caton, A.J.  
 submitted to the EMBL Data Library, April 1991  
 A:Reference number: S78449  
 A:Accession: S78449  
 A:Molecule type: mRNA  
 A:Residues: 1-60, 'T', 'S', '93-101 <CAT>  
 A:Cross-references: EMBL:X59193; NID:G52223; PIDN:CAA41903.1; PID:G1334067  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:8-88/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 0.44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 |||||  
 Db 48 WASTRES 54

## RESULT 13

A34153  
 Ig kappa chain V-IV region (Dep) - human  
 C:Species: Homo sapiens (man)

C:/Date: 11-Apr-1990 #sequence\_revision 11-Apr-1990 #text\_change 21-Jan-2000  
C:/Accession: A34153  
R/Mhaesco, E.; Ayadi, H.; Consy, N.; Gendron, M.C.; Roy, J.P.; Heyermann, H.; Frangione  
J. Biol. Chem. 264, 21481-21485, 1989  
A/Title: Multiple mutations in the variable region of the kappa light chains of three mc  
A/Reference number: A34153; MUID:90094313; PMID:2460953  
A/Accession: A34153  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-102 <MIH>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||  
Db 56 WASTRES 62

## RESULT 14

PH1047  
Ig light chain V region (clones 165.45 and 163-c1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C/Accession: PH1047; PH1049  
R/Tillman, D.M.; Jou, N.T.; Hill, R.T.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A/Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A/Reference number: PH0971; MUID:92381444; PMID:1512540  
A/Accession: PH1047  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-103 <TTL>  
A/Experimental source: B cell, strain [NZB x NZW]F1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||  
Db 56 WASTRES 62

## RESULT 15

PH1051  
Ig light chain V region (clone 165.3) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C/Accession: PH1051  
R/Tillman, D.M.; Jou, N.T.; Hill, R.T.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A/Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A/Reference number: PH0971; MUID:92381444; PMID:1512540  
A/Accession: PH1051  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-103 <TTL>  
A/Experimental source: B cell, strain [NZB x NZW]F1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WASTRES 7  
|||  
Db 56 WASTRES 62

Search completed: March 1, 2005, 17:44:46  
Job time : 9.47692 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:53 ; Search time 45.3385 Seconds  
(without alignments)  
79.062 Million cell updates/sec

Title: US-10-071-962-19  
Perfect score: 38  
Sequence: 1 WASTRES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	109	1 KV4D_HUMAN	P83593 homo sapien
2	38	100.0	114	1 KV4A_HUMAN	P01612 homo sapien
3	38	100.0	121	1 KV4O_HUMAN	P06312 homo sapien
4	38	100.0	133	1 KV4B_HUMAN	P06313 homo sapien
5	38	100.0	134	1 KV4C_HUMAN	P06314 homo sapien
6	35	92.1	130	2 Q9NP29	Q9NP29 homo sapien
7	34	89.5	934	2 Q6G2K3	Q6G2K3 bartonella
8	34	89.5	980	2 Q6R166	Q6R166 xanthomonas
9	33	86.8	266	2 Q6R165	Q6R165 homo sapien
10	33	86.8	1317	2 Q8TF23	Q8TF23 aspergillus
11	32	84.2	347	2 Q915J7	Q915J7 pseudomonas
12	32	84.2	458	2 Q7XU18	Q7XU18 oryza sativ
13	32	84.2	685	1 SYM_NEIMA	Q9JWP0 neisseria m
14	31	81.6	71	2 Q7QZC1	Q7QZC1 giardia lam
15	31	81.6	171	2 Q9MSV2	Q9MSV2 caenorhabdi
16	31	81.6	177	2 Q621F0	Q621F0 oryza sativ
17	31	81.6	183	2 Q57000	Q57000 zymomonas m
18	31	81.6	226	2 Q88087	Q88087 enterococcu
19	31	81.6	230	2 Q8NU75	Q8NU75 corynebacte
20	31	81.6	338	2 Q7ZQV2	Q7ZQV2 human immun
21	31	81.6	338	2 Q7ZQV3	Q7ZQV3 human immun
22	31	81.6	340	2 Q7ZQV5	Q7ZQV5 human immun
23	31	81.6	382	1 THRC_SYNY3	P74193 streptococc
24	31	81.6	404	1 YQ19_TREDE	Q73JF6 streptococc
25	31	81.6	404	2 Q9AMJ2	Q9AMJ2 streptococc
26	31	81.6	466	2 Q6AVV5	Q6AVV5 oryza sativ
27	31	81.6	504	2 Q64QF9	Q64QF9 bacteroides
28	31	81.6	564	2 Q9NA93	Q9NA93 caenorhabdi
29	31	81.6	572	2 Q92X10	Q92X10 rhizobium m
30	31	81.6	642	2 Q8RMG0	Q8RMG0 nosctoc sp.
31	31	81.6	642	2 Q8Z0C9	Q8Z0C9 anabaena sp

32	31	81.6	642	2 Q9ABQ5	Q9ABQ5 caulobacter
33	31	81.6	727	2 Q9BNW8	Q9BNW8 scutigerell
34	31	81.6	735	2 Q989J7	Q989J7 rhizobium l
35	31	81.6	783	2 Q8KJN0	Q8KJN0 rhizobium l
36	31	81.6	875	2 Q7RWP2	Q7RWP2 neuropept
37	31	81.6	1336	2 Q6WP53	Q6WP53 bdeliovibri
38	31	81.6	1499	2 Q9LH44	Q9LH44 arabidopsis
39	30	78.9	29	2 Q8C837	Q8C837 mus musculi
40	30	78.9	62	2 Q8B8F5	Q8B8F5 hepatitis b
41	30	78.9	78	2 Q8BW72	Q8BW72 mus musculi
42	30	78.9	94	2 Q7SEH6	Q7SEH6 neuropept
43	30	78.9	103	2 Q8Z272	Q8Z272 pyrobaculum
44	30	78.9	118	2 Q9BGP0	Q9BGP0 macaca fasc
45	30	78.9	119	2 Q8JY11	Q8JY11 hepatitis b

## ALIGNMENTS

RESULT 1					
ID	KV4D_HUMAN	STANDARD:	PRT:	109 AA.	
AC	P83593;				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Ig kappa chain V-IV region STR (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE.				
RC	TISU8=Abdominal adipose tissue;				
RX	MEDLINE=96249779; PubMed=9588180; DOI=10.1006/birc.1998.8515;				
RA	Olsen K.E., Sletten K., Westermarck P.;				
RT	"Extended analysis of AL-amyloid protein from abdominal wall				
RT	subcutaneous fat biopsy: kappa IV immunoglobulin light chain."				
RL	Biochem. Biophys. Res. Commun. 245:716-716(1998).				
CC	-I- FUNCTION: May play an important role in fibrillogenesis.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; TGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Direct protein sequencing; Immunoglobulin V region.				
FT	DOMAIN 1 23				
FT	DOMAIN 24 40				
FT	DOMAIN 41 55				
FT	DOMAIN 56 62				
FT	DOMAIN 63 94				
FT	DOMAIN 95 101				
FT	DOMAIN 102 109				
FT	DISULFID 23 94				
FT	UNSURE 23 23				
FT	UNSURE 94 94				
FT	NON_TER 109 109				
SQ	SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E2A0B CRC64;				
Query Match					
Best Local Similarity 100.0%; Score 38; DB 1; Length 109;					
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1 WASTRES 7					
DB 56 WASTRES 62					
RESULT 2					
ID	KV4A_HUMAN	STANDARD:	PRT:	114 AA.	
AC	P01625;				
DT	21-JUL-1986 (Rel. 01, Created)				

DT	01-OCT-1996 (Rel. 34, last sequence update)	
DR	25-OCT-2004 (Rel. 45, last annotation update)	
DE	ig kappa chain V-IV region Len.	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RA	SEQUENCE.	
RP	MEDLINE=76004342; PubMed=50995;	
RT	Schneider M., Hirschmann N.;	
RL	"The primary structure of a monoclonic immunoglobulin-L-chain of	
RR	subgroup IV of the kappa type (Bence-Jones protein Len).";	
RS	Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).	
RU	[2]	
RV	REVISION TO 9.	
SA	Salomon A.;	
SB	Submitted (AUG-1996) to Swiss-Prot.	
SC	-1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.	
CC	-1- MISCELLANEOUS: This is a Bence-Jones protein.	
DR	PDB; 1EEQ; X-ray; A/B=1-114.	
DR	PDB; 1EEU; X-ray; A/B=1-114.	
DR	PDB; 1EFQ; X-ray; A=1-114.	
DR	PDB; 1EK3; X-ray; A/B=1-114.	
DR	PDB; 1LVE; X-ray; @=1-114.	
DR	PDB; 3LVE; X-ray; @=1-114.	
DR	PDB; 5LVE; X-ray; A=1-114.	
DR	GO; GO:0005576; C:extracellular; NAS.	
DR	GO; GO:0003823; F:antigen binding; NAS.	
DR	GO; GO:0006955; P:immune response; NAS.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; Ig_Like; 1.	
DR	PROSITE; PS50835; IG_LIKE; 1.	
KW	3D-structure; Bence-Jones protein; Direct protein sequencing;	
KM	Immunoglobulin V region.	
FT	DOMAIN	1 23
FT	DOMAIN	24 40
FT	DOMAIN	41 55
FT	DOMAIN	56 62
FT	DOMAIN	63 94
FT	DOMAIN	95 101
FT	DOMAIN	102 113
FT	DISULFID	23 94
FT	STRAND	4 7
FT	STRAND	10 13
FT	TURN	15 16
FT	STRAND	19 25
FT	STRAND	30 31
FT	TURN	32 35
FT	STRAND	36 37
FT	STRAND	39 44
FT	TURN	46 47
FT	TURN	51 55
FT	TURN	56 58
FT	STRAND	59 60
FT	TURN	62 63
FT	TURN	66 67
FT	STRAND	68 73
FT	TURN	74 75
FT	STRAND	76 81
FT	HELIIX	86 88
FT	STRAND	90 96
FT	STRAND	103 104
FT	STRAND	108 112
FT	NON TER	114 114
Q	SEQUENCE	114 AA; 12640 MW; 0647F71D17F236485 CRC64;

QY	1	WASTRES	7
Db	56	WASTRES	62

RESULT 3	
KV40_HUMAN	
ID_KV40_HUMAN	STANDARD;
	PRT; 121 AA

DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE IG kappa chain V-IV region precursor (Fragment).  
GN Name:IGKV4-1;  
OS Homo sapiens (human).  
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN 111  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=66041853; PubMed=2997712;  
 RA Klobbeck H.G., Bornkamm G.W., Combrink R., Pohlentz H.D.,  
 Zachau H.G.,  
 RA "Subgroup IV of human immunoglobulin K light chains is encoded by a  
 RT single germ-line gene".  
 RT Nucleic Acids Res. 13:6515-6529(1985).  
 RL  
 CC -1- MISCELLANEOUS: There is only one Ig kappa V-IV gene.

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CC  
DR EMBL; Z00023; CAA77318.1; -.  
DR PIR; A01302; K4HU.  
DR HSSP; P01625; ILVE.  
DR Genew; HGNC:5834; IGKV4-1.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
DR Immunoglobulin V region; Signal.  
KW

FT	SIGNAL	1	20	Ig kappa chain V-IV region.
FT	CHAIN	21	>121	Framework-1.
FT	DOMAIN	21	43	Complementarity-determining-1.
FT	DOMAIN	44	60	Framework-2.
FT	DOMAIN	61	75	Complementarity-determining-2.
FT	DOMAIN	76	82	Framework-3.
FT	DOMAIN	83	114	Complementarity-determining-3.
FT	DOMAIN	115	121	By similarity.
FT	DISULFID	43	114	
FT	NON_TER	121	121	
EQ	SEQUENCE	121 AA;	13360 MW;	9566AD418BD33974 CRC64;

Query Match	100.0%	Score 38	DB 1	Length 121
Best Local Similarity	100.0%	Pred. No. 3.3		
Matches	7	Conservative	0	Indels 0
		Mismatches	0	Gaps 0
Qy	1	WASTRES	7	
db	76	WASTRES	82	

RESULT 4	
KV4B_HUMAN	
ID	STANDARD;
KV4B_HUMAN	PRT; 133 AA

```

AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combic G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529 (1985).
CC -----
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CC -----
CC EMBL: Z00022; CAA7317.1; -.
DR PIR: A01904; K4HUI1.
DR HSSP: P01625; LIVE.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KM
FT CHAIN 1 133
FT DOMAIN 21 43 Ig kappa chain V-IV region JI.
FT DOMAIN 44 60 Framework-1.
FT DOMAIN 61 75 Complementarity-determining-1.
FT DOMAIN 76 82 Framework-2.
FT DOMAIN 83 114 Complementarity-determining-2.
FT DOMAIN 115 122 Framework-3.
FT DOMAIN 123 132 Complementarity-determining-3.
FT DISULFID 43 114 Framework-4.
FT NON TER 133 By similarity.
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 76 WASTRES 82

RESULT 5
KV4C HUMAN STANDARD; PRT; 134 AA.
ID P06314;
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA March P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe."
RL Nucleic Acids Res. 13:6531-6544 (1985).
RN [2]
RP REVISION TO 76.
RA March P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL: X02990; CAA2673.1; -.
DR HSSP: P01625; LIVE.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KM
FT CHAIN 1 134
FT DOMAIN 21 43 Ig kappa chain V-IV region B17.
FT DOMAIN 44 60 Framework-1.
FT DOMAIN 61 75 Complementarity-determining-1.
FT DOMAIN 76 82 Framework-2.
FT DOMAIN 83 114 Complementarity-determining-2.
FT DOMAIN 115 121 Framework-3.
FT DOMAIN 122 133 Complementarity-determining-3.
FT DISULFID 43 114 Framework-4.
FT NON TER 134 By similarity.
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD078832 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
DB 76 WASTRES 82

RESULT 6
Q9NP29 PRELIMINARY; PRT; 130 AA.
ID Q9NP29;
AC Q9NP29;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Microfibrillar protein 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96354815; PubMed=8753791; DOI=10.1006/dbrc.1996.1202;
RA Ozsvath K.J., Xia S., Hirose H., Tilson M.D.;
RT "Two hypothetical proteins of human aortic adventitia, with Ig kappa,
RT collagenous, and aromatic-rich motifs."
RL Biochem. Biophys. Res. Commun. 225:500-504 (1996).
RN [2]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97367690; PubMed=9224393; DOI=10.1006/jvire.1997.19030;  
 RA Oszvath K.J., Hirose H., Xia S., Chew D., Knoetgen J. III,  
 RA Tilson M.D.;  
 RT "Expression of two novel recombinant proteins from aortic adventitia  
 RT (kappa) sharing amino acid sequences with cytomegalovirus.";  
 RL J. Surg. Res. 63:277-282(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Oszvath K.J., Xia S., Hirose H., Tilson M.D.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF206020; AAF62402.1; -  
 DR HSSP; P01625; IIVE.  
 DR InterPro; IPR007110; 1g-like.  
 FT NON TER 130 130  
 SQ SEQUENCE 130 AA; 14128 MW; 51275185XCGFAIE CRC64;  
 Query Match 92.1%; Score 35; DB 2; Length 130;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 WASTRE 7  
 Db 76 WASTRDS 82  
 RESULT 7  
 ID 06G2K3 PRELIMINARY; PRT; 934 AA.  
 AC 06G2K3;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocuNames=BH11960;  
 OS Bartonella henselae (Rochalimaea henselae).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bartonellaceae; Bartonella.  
 OX NCBI\_TaxID=38323;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 49882 / Houston 1;  
 RX PubMed=15210978; DOI=10.1073/pnas.0305659101;  
 RA Alsmark U.C.M., Frank A.C., Kariberg E.O., Legault B.-A., Ardell D.H.,  
 RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvel M.,  
 RA La Scola B., Holmberg M., Anderson S.G.E.;  
 RT "The louse-borne human pathogen Bartonella quintana is a genomic  
 RT derivative of the zoonotic agent Bartonella henselae.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).  
 DR EMBL; BX897699; CAF27979.1; -  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 934 AA; 104092 MW; 238F0F60D2D5BF19 CRC64;  
 Query Match 89.5%; Score 34; DB 2; Length 934;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 WASTRE 6  
 Db 98 WASTRE 103  
 RESULT 8  
 ID 08PL66 PRELIMINARY; PRT; 980 AA.  
 AC 08PL66;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE GDEF family protein.  
 GN OrderedLocuNames=XAC1940;  
 OS Xanthomonas axonopodis (pv. citri).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.

OX NCBI\_TaxID=92829;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=306 / ATCC 13902 / XV 101;  
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
 RA Camarotte G., Camavari F., Cardozo J., Chambergo F., Clapina L.P.,  
 RA Ciccarelli R.M.B., Coutinho L.B., Cursino-Santos J.R., El-Dorry H.,  
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Tundade dos Santos W., Truffi D., Tsai S.W., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities";  
 RL Nature 417:459-463(2002).  
 DR EMBL; AE011829; AAM36802.1; -  
 DR InterPro; IPR000160; GDEF.  
 DR InterPro; IPR011110; Reg\_prop.  
 DR InterPro; IPR011123; Y\_Y.  
 DR Pfam; PF00990; GDEF; 1.  
 DR Pfam; PF07494; Reg\_prop; 10.  
 DR Pfam; PF07495; Y\_Y; 1.  
 DR SMART; SM00267; DUF1; 1.  
 DR TIGRFAMs; TIGR00254; GDEF; 1.  
 DR PROSITE; PSS0887; GDEF; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 980 AA; 107940 MW; 47179C81E6DCE442 CRC64;  
 Query Match 89.5%; Score 34; DB 2; Length 980;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 WASTRE 6  
 Db 492 WASTRE 497  
 RESULT 9  
 ID 06P0U5 PRELIMINARY; PRT; 266 AA.  
 AC 06P0U5;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong D.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarekne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Vallian D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Mair M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011643; AAH11643.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 266 AA; 29322 MW; 5DE33CA2D1AD11A4 CRC64;

Query Match  
 Best Local Similarity 86.8%; Score 33; DB 2; Length 266;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 Db 249 WASNRES 255

RESULT 10  
 08TFZ3 PRELIMINARY; PRT; 1317 AA.  
 ID 08TFZ3;  
 AC 08TFZ3;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=Alfa35g10.09C;  
 OS Aspergillus fumigatus (Sartorya fumigata).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 OX NCBI\_TaxID=5085;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14998527; DOI=10.1016/j.fgb.2003.12.003;  
 RA Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins M.,  
 RA Foster N., Fraser A., Harris D., Larke N., Murphy L., Humphrey S.,  
 RA O'Neill S., Pertea M., Price C., Rabinowitch B., Rajandream M.A.,  
 RA Salzberg S., Saunders D., Seegar K., Sharp S., Warren T.,  
 RA Denning D.W., Batteil B., Hall N.;  
 RT "Insight into the genome of Aspergillus fumigatus: analysis of a 922  
 RT kb region encompassing the nitrate assimilation gene cluster.";  
 RL Fungal Genet. Biol. 41:443-453(2004).  
 CC -1- SIMILARITY: Contains 3 WD repeats.  
 DR EMBL; BX649606; CAD29602.1; -  
 DR InterPro; IPR001680; WD40.  
 DR InterPro; IPR011046; WD40\_1like.  
 DR Pfam; PF00400; WD40\_3.  
 DR SMART; SM00320; WD40\_3.  
 KW Hypothetical protein; Repeat; WD repeat.  
 SQ SEQUENCE 1317 AA; 148645 MW; 0DC4B0BD19A45DE CRC64;

Query Match  
 Best Local Similarity 86.8%; Score 33; DB 2; Length 1317;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 Db 979 WASNRES 985

RESULT 11  
 0915J7 PRELIMINARY; PRT; 347 AA.  
 AC 0915J7;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=PA0732;  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,  
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,  
 RA Gaeber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lapidis K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizner J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 405:959-964(2000).  
 DR EMBL; AE004508; AAG04121.1; -  
 DR PIR; D83554; D83554.  
 DR InterPro; IPR005490; ERFK\_Ybis\_YnG.  
 DR Pfam; PF03734; ERFK\_Ybis\_YnG\_1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 347 AA; 37161 MW; 264E4DC064230CC3 CRC64;

Query Match  
 Best Local Similarity 84.2%; Score 32; DB 2; Length 347;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WASTRES 7  
 Db 318 WASTRDT 324

RESULT 12  
 07XU18 PRELIMINARY; PRT; 458 AA.  
 ID 07XU18;  
 AC 07XU18;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE OSUNBD0103108.17 protein.  
 GN Name=OSUNBD0103108.17;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12447439; DOI=10.1038/nature01183;  
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,  
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,  
 RA Weng Q., Zhang L., Li Y., Wu Y., Lu Y., Zhang L.S., Yu Z., Fan D.,  
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,  
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,  
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,  
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,  
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,  
 RA Lan L., Lai Y., Cheng Z., Gu W., Jiang J., Li J., Hong G., Xue Y.,  
 RA Han B.;  
 RT "Sequence and analysis of rice chromosome 4.";  
 RL Nature 420:316-320(2002).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AL606635; CAD41278.2; -  
 DR Gramene; 07XU18; -  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.

Qy	Db	Query Match	Similarity	Score 32;	DB 2;	Length 458;
		Beet Local	Similarity	85.7%;	Pred. No. 2.6e+02;	
		Matches	6;	Conservative	0;	Mismatches 1;
					Indels	0;
					Gaps	0;
Qy	1	WASTRES 7				
	59	WASTRPS 65				
Db						
RESULT 13						
SYM_NEIMA	STANDARD;	PRT;	685 AA.			
AC	Q9JMP0;					
DT	28-FEB-2003 (Rel. 41, Created)					
DT	28-FEB-2003 (Rel. 41, Last sequence update)					
DT	25-OCT-2004 (Rel. 45, Last annotation update)					
DE	Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase) (MetRS).					
OS	Name=metG; OrderedLocustNames=NMA0275;					
OC	Neisseria meningitidis (serogroup A).					
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;					
OC	Neisseriaceae; Neisseria.					
OX	NCBI_TaxID=65699;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Z2491 / Serogroup A / Serotype 4A;					
RC	MEBLIN=20222556; PubMed=10761919; DOI=10.1038/35006555;					
RA	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,					
RA	Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,					
RA	Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holtroyd S.,					
RA	Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,					
RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,					
RA	Whitehead S., Spratt B.G., Barrall B.G.;					
RT	"Complete DNA sequence of a serogroup A strain of Neisseria					
RT	meningitidis Z2491".					
RL	Nature 404:502-506(2000).					
CC	-1- FUNCTION: Is required not only for elongation of protein synthesis					
CC	but also for the initiation of all mRNA translation through					
CC	initiator tRNA(Emet) aminoacylation (By similarity).					
CC	-1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +					
CC	diphosphate + L-methionyl-tRNA(Met).					
CC	-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).					
CC	-1- SUBUNIT: Homodimer (By similarity).					
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.					
CC	-1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase					
CC	family. MetG subfamily 1.					
CC	-1- SIMILARITY: Contains 1 tRNA-binding domain.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC	the European Bioinformatics Institute. There are no restrictions on its					
CC	use by non-profit institutions as long as its content is in no way					
CC	modified and this statement is not removed. Usage by and for commercial					
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>					
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).					
CC	-----					
CC	EMBL; AL162752; CAB83583.1; -					
CC	PIR; G82022; G82022.					
CC	-----					

```

DR HSSP; P00959; IMEA.
DR HAMAP; MF_00098; fused; 1.
DR InterPro; IPR004495; MetG_Cterm.
DR InterPro; IPR008224; MetR_dimerising.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt_met.
DR InterPro; IPR002547; tRNA_bind.
DR InterPro; IPR009080; tRNAsyn_1a_bind.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF001528; MetRS_dimerising; 1.
DR PRINTS; PRIO141; TRNASYNTHET.
DR TIGRFAMs; TIGR00398; metG; 1.
DR TIGRFAMs; TIGR00399; metG_C term; 1.
DR PROSITE; PS00179; AA tRNA_LIGASE_I; 1.
DR PROSITE; PS50886; TRBD; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Metal-binding; Protein biosynthesis; RNA-binding; tRNA-binding; Zinc.
FT SITE 12 22 "HIGH" region.
FT SITE 12 22 "KMSKS" region.
FT DOMAIN 339 343 tRNA-binding.
FT METAL 143 143 Zinc (By similarity).
FT METAL 146 146 Zinc (By similarity).
FT METAL 156 156 Zinc (By similarity).
FT METAL 159 159 Zinc (By similarity).
FT BINDING 342 342 ATP (By similarity).
SQ SEQUENCE 685 AA; 76984 MW; 07FD45915ED3BEF3 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 685;
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 520 WANTRET 526

RESULT 14
O7OYC1 PRELIMINARY; PRT; 71 AA.
ID O7OYC1
AC O7OYC1;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE GLP 387 11136 11351.
OS Giardia_lambila ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
CX NCBI_TaxID=164922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB C6;
RA Morrison H.G., McCarthy A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RL "Draft sequence of the Giardia lambila genome."
CC Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL; AACB0100052; EAA40034.1; -.
SQ SEQUENCE 71 AA; 8127 MW; 0374829B52C40BE3 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 71;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WASTRES 7
Db 65 WASSROS 71

RESULT 15

```

O9NSV2  
ID O9NSV2 PRELIMINARY; PRT: 171 AA.  
AC O9NSV2;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Hypothetical protein CC8.1.  
GN Name=CC8.1; ORFNames=CC8.1;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG WormBase Consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RT "The sequence of C. elegans cosmid CC8.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC006626; AAF39788.1; -.  
DR InAct; O9NSV2;  
DR WormBase; WBGene0016986; CC8.1.  
DR WormPep; CC8.1; CE20616.  
KW Hypothetical protein.  
SQ SEQUENCE 171 AA; 17643 MW; 03AD996B9A627CFD CRC64;

Db 122 MATTRE 127

Search completed: March 1, 2005, 17:43:19  
Job time : 47.3385 secs

Query Match 81.6%; Score 31; DB 2; Length 171;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 WASTRE 6

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: March 1, 2005, 17:16:08 ; Search time 59.8154 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-10-071-962-20

Perfect score: 41

Sequence: 1 KQSYNLRT 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database : A Geneseq\_16Dec04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	8	3	AAV32228
2	41	100.0	114	2	AAV06630
3	41	100.0	148	1	AAV93078
4	41	100.0	219	2	AAV44495
5	41	100.0	265	2	AAV52864
6	36	87.8	84	2	AAW14491
7	36	87.8	84	2	AAV9878
8	35	85.4	8	2	AAV76084
9	35	85.4	219	2	AAV76086
10	35	85.4	239	2	AAV76087
11	35	85.4	288	2	AAV82743
12	35	85.4	673	2	AAV82742
13	34	82.9	249	2	AAV60770
14	33	80.5	8	2	AAV70910
15	33	80.5	18	2	AAV70916
16	33	80.5	110	2	AAV56520
17	33	80.5	110	2	AAV56517
18	32	78.0	166	4	AAU71926
19	32	78.0	318	5	AAE20107
20	32	78.0	453	5	ABR09487
21	31	75.6	37	5	AAE23239
22	31	75.6	114	7	AAV06631
23	31	75.6	161	7	ADC95923
24	31	75.6	283	2	AAW93214
25	31	75.6	370	7	ADF69092

26	31	75.6	422	6	ABU41136	Abu41136 Protein e
27	31	75.6	424	7	ADF06925	Adf06925 Bacterial
28	31	75.6	437	4	AAV62618	AAV62618 Petunia z
29	31	75.6	437	4	AAV64524	AAV64524 P. hybrid
30	31	75.6	437	7	ADD02815	ADD02815 Petunia h
31	31	75.6	437	8	ADF38736	Adf38736 Petunia x
32	31	75.6	539	8	ADL00081	ADL00081 Streptoco
33	31	75.6	541	5	AAE23235	AAE23235 Streptoco
34	31	75.6	542	8	ADL00082	ADL00082 Streptoco
35	31	75.6	542	8	ADL00077	ADL00077 Streptoco
36	31	75.6	542	8	ADL00079	ADL00079 Streptoco
37	31	75.6	542	8	ADL00083	ADL00083 Streptoco
38	31	75.6	542	8	ADL00084	ADL00084 Streptoco
39	31	75.6	542	8	ADL00080	ADL00080 Streptoco
40	31	75.6	542	8	ADL00085	ADL00085 Streptoco
41	31	75.6	542	8	ADL00078	ADL00078 Streptoco
42	31	75.6	542	8	ADL00086	ADL00086 Streptoco
43	31	75.6	543	5	ABP29881	ABP29881 Streptoco
44	31	75.6	543	8	ADL00076	ADL00076 Streptoco
45	31	75.6	543	8	ADL010465	ADL010465 Group B S

## ALIGNMENTS

RESULT 1	AAV32228	AAV32228 standard; peptide; 8 AA.
AC	AAV32228;	
DT	15-FEB-2000	(first entry)
DE	G-CSF agonist antibody mAb163-93 light chain variable region CDR3.	
DE	Granulocyte colony stimulating factor receptor; G-CSF; mouse;	
KW	monoclonal antibody; agonist; screening; neutropenia; therapy;	
KW	complementarity determining region; CDR; mAb163-93.	
OS	Mus musculus.	
PN	W0955735-A1.	
PD	04-NOV-1999.	
PF	30-APR-1999;	99WO-US009466.
PR	30-APR-1998;	98US-0083575P.
PA	(TANNO-) TANOX INC.	
PI	Ni B, Sun BNC, Sun CRX;	
DR	WPI; 2000-052805/04.	
PT	Treatment of neutropenia by stimulating proliferation of neutrophilic	
PT	cell lineage progenitors.	
PS	Claim 13; Page 30; 64pp; English.	
CC	The present sequence represents complementarity determining region 3	
CC	(CDR3) of the light chain variable region of murine monoclonal antibody	
CC	mAb163-93. This antibody is an example of an agonist molecule that	
CC	specifically binds to or interacts with human granulocyte colony	
CC	stimulating factor (G-CSF) receptor to stimulate cell proliferation and	
CC	differentiation, especially by dimerizing the receptor or activating	
CC	phosphorylation of kinases associated with the receptor or activating	
CC	antibodies can be used to stimulate proliferation of G-CSF-dependent	
CC	cells, e.g. to differentiate leading to a repopulation of neutrophilic	
CC	granulocyte lineage cells, especially to treat neutropenia (claimed).	
CC	They can also be used to detect human G-CSF receptor immunologically	
SO	Sequence 8 AA;	

Query Match 100.0%; Score 41; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
 |||||  
 1 KOSYNLRT 8

RESULT 2  
 ID AAY06830 standard; protein; 114 AA.

AC AAY06830;  
 XX 25-JUN-1999 (first entry)  
 DE Mouse Mab 6A4 light chain variable region.

XX Rolling template; nucleic acid synthesis; polynucleotide polymerase;  
 KM gene production; primer; monoclonal antibody; 6A4; ss.

XX Mus sp.

XX MO9914370-A1.

XX 25-MAR-1999.

XX 15-SEP-1998; 98WO-US019157.

XX 15-SEP-1997; 97US-00929856.

XX (HIAT/) HIATT A C.  
 XX (ROSE/) ROSE F D.

XX Hiatt AC, Rose FD;

XX WPI; 1999-244045/20.

XX N-PSDB; AAX34465.

XX Producing specific polynucleotides using rolling templates.

XX Example 6; Page 75; 109pp; English.

XX The invention relates to a method for producing polynucleotides having a  
 CC defined sequence using rolling templates that successively add  
 CC nucleotides (nts) to a longer primer strand. The method comprises: (i)  
 CC incubating, under annealing conditions, a primer and a template that has  
 CC a 5'-region not complementary to the primer, a 3'-region complementary to  
 CC the 3'-end of primer and a non-reactive 3'-terminus, with the template  
 CC being shorter than the primer; (ii) reacting the primer with at least one  
 CC nt in presence of a template-dependent polynucleotide polymerase to  
 CC extend it by at least one nt (complementary to the 5'-region of template)  
 CC at its 3'-end; (iii) separating the template and the extended primer; and  
 CC (iv) repeating the cycle of (i)-(iii) as often as needed to synthesize  
 CC the desired polynucleotide. The method is especially used to produce  
 CC genes or their segments. The method provides fast, accurate, inexpensive  
 CC synthesis of RNA or DNA and is more efficient than chemical coupling  
 CC processes. It has higher specificity and eliminates the need for  
 CC deprotection. The products can be cloned directly. The method avoids  
 CC problems of waste disposal and includes an inherent editing effect  
 CC (failure sequences will not be extended further in subsequent rounds) so  
 CC that purification of the end product is facilitated. Synthesis may take  
 CC place on a vector, simplifying cloning and sequences with codon usage  
 CC optimized for a particular host can be prepared. This represents the  
 CC amino acid sequence of the light chain variable region of the mouse  
 CC monoclonal antibody (Mab) 6A4, synthesized by the method of the invention  
 XX Sequence 114 AA;

Query Match 100.0%; Score 41; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KOSYNLRT 8  
 |||||  
 95 KOSYNLRT 102

RESULT 3  
 ID AAP93078 standard; peptide; 148 AA.

AC AAP93078;

XX 25-MAR-2003 (revised)

XX 31-OCT-2002 (revised)

XX 14-MAR-1990 (first entry)

XX Light chain of monoclonal antibody 6A4.

XX Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.

XX Unidentified.

XX EP38395-A.

XX 25-OCT-1989.

XX 12-APR-1989; 89EP-00106463.

XX 19-APR-1988; 88DE-03813023.

XX (BEHW) BEHRINGER AG.

XX Domdey H, Marget M, Vonspecht B;

XX WPI; 1989-310861/43.

XX N-PSDB; AAN91663.

XX Monoclonal antibody to pseudomonas aeruginosa - and DNA coding for  
 PT variable antibody regions.

XX Claim 1; Page 6; 7pp; German.

XX The peptide is encoded by the light chain of monoclonal antibody 6A4. 6A4  
 CC reacts with the OMP-1 protein of all 19 known serotypes of P. aeruginosa.  
 CC It is used for therapy and diagnosis of infection, and as a carrier for  
 CC drugs. The antibody is IgG2a subclass. (Updated on 31-OCT-2002 to add  
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated  
 CC on 25-MAR-2003 to correct PI field.)  
 XX

XX Sequence 148 AA;

Query Match 100.0%; Score 41; DB 1; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
 |||||  
 115 KOSYNLRT 122

RESULT 4  
 ID AAR44495 standard; protein; 219 AA.

AC AAR44495;

XX 25-MAR-2003 (revised)

XX 26-MAY-1994 (first entry)

XX Sequence of the immunoglobulin IgG (1G3/86) kappa chain derived from  
 DE clone gamma1.1a and augmented using PCR.  
 XX

KW Particle-binding antibody fragment; kappa chain;  
 KW monoclonal cell line IC3/86; anti-erythrocyte IgGs.  
 OS Synthetic.  
 XX MO9324630-A1.  
 XX  
 XX  
 XX  
 XX PD 09-DEC-1993.  
 XX PF 19-MAY-1993; 93WO-AU000228.  
 XX PR 22-MAY-1992; 92AU-00002551.  
 XX  
 XX (AGEN-) AGEN LTD.  
 XX  
 XX Lilliey GG, Hudson PJ, Hillyard CJ;  
 XX WPI; 1993-405821/50.  
 XX DR N-PSDB; AA053430.  
 XX  
 XX Bifunctional recombinant protein - contains particle and analyte binding  
 PT moieties, used in agglutination assays pref. on whole blood.  
 XX  
 XX Example; Fig 2; 42pp; English.  
 XX  
 XX mRNA was prep'd. from monoclonal antibody cell line (IC3/86) which prods  
 CC anti-erythrocyte IgGs which bind to RBCs. de-cDNA was prep'd. and cloned  
 CC into lambda-g10 arms and packaged into a phage library. The heavy chain  
 CC clone gamma-W/1.1 and the light chain clone ph76-kappa-10 were used to  
 CC source ds-DNA inserts for the screening of the g10 library. Positive  
 CC clones were amplified, and the positive insert cDNA subcloned into pUC18.  
 CC As a result a near full-length gamma clone (gamma-1.1a) was identified,  
 CC the nucleotide sequence was determined and from this the protein sequence  
 CC deduced (AA053429/R4494). The sequences of a partial kappa clone (kappa-  
 CC 4A1) which encoded the 3' end of the variable domain and full constant  
 CC domain were determined in a similar fashion. To determine the sequence of  
 CC the IC3/86 kappa light chain at the 5' end, a mixed N-terminal sequence  
 CC was determined from the intact IC3/86 Ig and together with the sequence  
 CC from a gamma heavy chain clone used to determine the N-terminus of the  
 CC variable region of the kappa light chain. A coding sequence for this  
 CC amino acid sequence was compiled and PCR amplified using the redundant  
 CC forward (sense) primer N960 and the reverse (antisense) primer N852)  
 CC which was based on the kappa constant region beginning at nucleotide 337  
 CC (see AA053430). The sequences derived from the PCR and g10 library  
 CC enabled the compilation of the sequence in AA053430. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 CC  
 XX  
 XX SQ Sequence 219 AA;  
 XX  
 XX Query Match 100.0%; Score 41; DB 2; Length 219;  
 XX Best Local Similarity 100.0%; Pred. No. 3.3;  
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 KOSYNLRT 8  
 XX |||||  
 XX Db 95 KOSYNLRT 102  
 XX  
 XX  
 XX RESULT 5  
 XX AAR52864  
 XX ID AAR52864 standard; protein; 265 AA.  
 XX  
 XX AC AAR52864;  
 XX  
 XX XX 27-AUG-2003 (revised)  
 XX DT 25-MAR-2003 (revised)  
 XX DT 09-SEP-1994 (first entry)  
 XX  
 XX DE Glycophorin antibody IC3 scFv.  
 XX  
 XX KW Glycophorin; antibody IC3; target binding polypeptide; PCR;  
 KW polymerase chain reaction; primer; scFv; single chain antibody;  
 KW phagemid pHPA; vector; antibody engineering; humanized antibody.

XX  
 OS Unidentified.  
 XX  
 XX MO9407921-A1.  
 XX  
 XX  
 XX PD 14-APR-1994.  
 XX  
 XX PF 24-SEP-1993; 93WO-AU000491.  
 XX PR 25-SEP-1992; 92AU-00004973.  
 XX  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX  
 XX PI Hudson PJ, Lah M, Kortt A, Irving RA, Atwell JL, Malby RL;  
 XX PI Power BE, Colman PM;  
 XX WPI; 1994-135515/16.  
 XX DR N-PSDB; AA062956.  
 XX  
 XX PT New target-binding polypeptide(s) used for diagnosis, etc. - having a  
 PT stable core polypeptide region with at least one target-binding region  
 PT covalently attached, pnt. mutated to alter specificity, etc.  
 XX  
 XX PS Disclosure; Page 40; 67pp; English.  
 XX  
 XX PCR primers N2034 (AA062947) and N2035 (AA062948) were used with anti-  
 CC glycophorin IC3 antibody template DNA in a PCR to produce a IC3 product  
 CC of 3'-VN sequence juxtaposed to 5'-VN sequence flanked by BstEII and NotI  
 CC sites. Products were ligated with vector pHPA containing a IC3 scFv  
 CC sequence, and expressed in Escherichia coli TGI. The DNA sequence of the  
 CC linkerless IC3 scFv in pHPA is given in AA062956 (encoding protein  
 CC AAR52864). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-  
 CC MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS  
 CC field.)  
 CC  
 XX  
 XX SQ Sequence 265 AA;  
 XX  
 XX Query Match 100.0%; Score 41; DB 2; Length 265;  
 XX Best Local Similarity 100.0%; Pred. No. 4;  
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 KOSYNLRT 8  
 XX |||||  
 XX Db 236 KOSYNLRT 243  
 XX  
 XX  
 XX RESULT 6  
 XX AAW14491  
 XX ID AAW14491 standard; protein; 84 AA.  
 XX  
 XX AC AAW14491;  
 XX  
 XX DT 25-MAR-2003 (revised)  
 XX DT 28-JAN-1997 (first entry)  
 XX  
 XX DE Monoclonal antibody D VK.  
 XX  
 XX KW heavy; light chain; monoclonal antibody; antigen 3; marker; melanoma;  
 KW permanent human tumour cell line; tumour-associated antigen; epitope;  
 KW gastrointestinal tumour; pancreatic carcinoma; diagnostic; therapeutic;  
 KW antigen 11; Vibrio cholera; neuraminidase-resistant; ganglioside GD2.  
 XX  
 XX OS Synthetic.  
 XX  
 XX XX EP727436-A1.  
 XX PN 21-AUG-1996.  
 XX PD 21-AUG-1996.  
 XX  
 XX PF 21-MAR-1990; 96EP-00100443.  
 XX  
 XX XX 24-MAR-1989; 89DE-003909799.  
 XX PR 21-MAR-1990; 90EP-00105322.  
 XX

PA (BEHW ) BEHRINGWERKE AG.  
 XX Bosslet K, Seemann G, Sedlacek H, Auerbach B;  
 XX WPI; 1996-372836/38.  
 DR N-PSDB; AAT63508.  
 XX  
 PT Monoclonal antibody to tumour-associated antigen - useful as  
 PT gastrointestinal tumour marker.  
 XX  
 PS Disclosure; Page 14; 19pp; German.  
 CC AAM14490-91 are the heavy and light chains (respectively) of monoclonal  
 CC antibody (Mab) D. Mab D recognises Vibrio cholera neuraminidase-resistant  
 CC epitope of ganglioside GD2, from a human melanoma cell line. Mabs A, B  
 CC and C (see AAM14484-89) are mentioned in the specification, but are not  
 CC part of the claims. Mabs A and B recognise antigens 3 and 11 resp., of a  
 CC permanent human tumour cell line. Mab C also recognises an epitope of a  
 CC tumour-associated antigen. These antigens occur at high concns. in the  
 CC serum of patients with gastrointestinal tumours, e.g. pancreatic  
 CC carcinoma, and are thus useful as tumour markers for diagnostic or  
 CC therapeutic purposes. (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC  
 SQ Sequence 84 AA;  
 QY 1 KQSYNLR 7  
 DB 67 KQSYNLR 73  
 OY 1 KQSYNLR 7  
 DB 67 KQSYNLR 73  
 RESULT 7  
 AAR9878 AAR9878 standard; protein; 84 AA.  
 XX  
 AC AAR9878;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-JUN-1997 (first entry)  
 XX  
 DE Monoclonal antibody D VK.  
 XX  
 KM Monoclonal antibody; Mab; epitope; tumour-associated antigen; marker;  
 KM antigen.  
 XX  
 OS Synthetic.  
 XX  
 PN EP2727435-A1.  
 XX  
 PD 21-AUG-1996.  
 XX  
 PF 21-MAR-1990; 96EP-00100442.  
 XX  
 PR 24-MAR-1989; 89DE-03909799.  
 PR 21-MAR-1990; 90EP-00105322.  
 XX  
 PA (BEHW ) BEHRINGWERKE AG.  
 XX  
 XX Bosslet K, Seemann G, Sedlacek H, Auerbach B;  
 XX WPI; 1996-372836/38.  
 DR N-PSDB; AAT63666.  
 XX  
 PT Monoclonal antibody to tumour-associated antigen - useful as  
 PT gastrointestinal tumour marker.  
 XX  
 PS Disclosure; Page 14; 19pp; German.  
 CC Mab C (AAT63659-T63660) is a monoclonal antibody that recognises an

CC epitope of a tumour-associated antigen occurring at high concn. in the  
 CC serum of patients with gastrointestinal tumours, e.g. pancreatic  
 CC carcinoma, and is thus useful as a tumour marker for diagnostic or  
 CC therapeutic purposes. Mabs A, B and D are mentioned in the specification,  
 CC but are not part of the claims. Mab A (AAT6661-T6662) recognises  
 CC antigen 3 of permanent human tumour cell line. Mab B (AAT6663-T6666)  
 CC recognises antigen 11 of permanent human tumour cell line. Mab D  
 CC (AAT6665-T6666) recognises a Vibrio cholera neuraminidase-resistant  
 CC epitope of ganglioside GD2, from a human melanoma cell line. (Updated on  
 CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.)  
 CC  
 SQ Sequence 84 AA;  
 QY 1 KQSYNLR 7  
 DB 67 KQSYNLR 73  
 OY 1 KQSYNLR 7  
 DB 67 KQSYNLR 73  
 RESULT 8  
 AAR76084 AAR76084 standard; peptide; 8 AA.  
 XX  
 AC AAR76084;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-NOV-1995 (first entry)  
 XX  
 DE Mab 55.1 light chain CDR3.  
 XX  
 KM Antigen binding structure; complementarily determining region; CDR;  
 KM CA55.1; colorectal cancer; tumour-associated antigen; hybridoma;  
 KM monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;  
 KM transgenic animal; transgenic plant; antibody engineering;  
 KM humanized antibody; immunotoxin.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9515382-A1.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 29-NOV-1994; 94WO-GB002610.  
 XX  
 PR 03-DEC-1993; 93GB-00024819.  
 PR 03-JUN-1994; 94GB-00011089.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF,  
 PI Blakey DC;  
 XX  
 DR WPI; 1995-215262/28.  
 XX  
 PT Antigen binding structures containing CDR's recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
 PT and therapy of cancer.  
 XX  
 PS Claim 2; Page 97; 121pp; English.  
 XX  
 CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
 CC of the heavy and light chains of Mab 55.1 (ECCAC 93081901), which  
 CC recognises the colorectal tumor-associated antigen CA55.1. It is  
 CC optionally humanized and in the form F(ab')<sub>2</sub>, F(ab)'', Fab, scFv or V-  
 CC min, and is produced in transgenic animals or plants. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 CC  
 SQ Sequence 8 AA;

Query Match 85.4%; Score 35; DB 2; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8  
 |||||  
 XX 1 KOSYTLRT 8

RESULT 9  
 AAR76086  
 ID AAR76086 standard; peptide; 219 AA.  
 AC AAR76086;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-NOV-1995 (first entry)  
 DE MAb 55.1 light chain.  
 XX  
 KW Antigen binding structure; complementarity determining region; CDR;  
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
 KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
 KW transgenic animal; transgenic plant; antibody engineering;  
 KW humanized antibody; immunotoxin.  
 XX  
 OS Mus sp.  
 XX  
 PN W09515382-A1.  
 PD 08-JUN-1995.  
 XX  
 PE 29-NOV-1994; 94WO-GB002610.  
 XX  
 PR 03-DEC-1993; 93GB-00024819.  
 PR 03-JUN-1994; 94GB-00011089.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
 PI Blakey DC;  
 XX  
 DR WPI; 1995-215262/28.  
 XX  
 PT Antigen binding structures containing CDR's recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
 PT and therapy of cancer.  
 PS Claim 3; Page 98; 121pp; English.  
 XX  
 CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
 CC of the heavy (AAR76085) and light (AAR76086) chains of MAb 55.1 (ECACC  
 CC 93081901), which recognises the colorectal tumor-associated antigen  
 CC CA55.1. It is optionally humanized and in the form F(ab)'2, F(ab)', Fab,  
 CC Fv, scFv or V-min, and is produced in transgenic animals or plants.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SQ Sequence 219 AA;

Query Match 85.4%; Score 35; DB 2; Length 219;  
 Best Local Similarity 87.5%; Pred. No. 55;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8  
 |||||  
 Db 95 KOSYTLRT 102

RESULT 10  
 AAR76087  
 ID AAR76087 standard; protein; 239 AA.  
 XX  
 AC AAR76087;

XX 25-MAR-2003 (revised)  
 DT 21-NOV-1995 (first entry)  
 DE MAb 55.1 light chain.  
 XX  
 KW Antigen binding structure; complementarity determining region; CDR;  
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
 KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
 KW transgenic animal; transgenic plant; antibody engineering;  
 KW humanized antibody; immunotoxin.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= sig\_peptide  
 FT Protein 21..239  
 FT /label= Mat\_protein  
 FT /note= "claim 3, page 98"

W09515382-A1.  
 PD 08-JUN-1995.  
 XX  
 PE 29-NOV-1994; 94WO-GB002610.  
 XX  
 PR 03-DEC-1993; 93GB-00024819.  
 PR 03-JUN-1994; 94GB-00011089.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
 PI Blakey DC;  
 XX  
 DR WPI; 1995-215262/28.  
 DR N-PSDB; AAQ94036.  
 XX  
 PT Antigen binding structures containing CDR's recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
 PT and therapy of cancer.  
 PS Disclosure; Fig 16; 121pp; English.  
 XX  
 CC MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated  
 CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)  
 CC chains of 55.1 were isolated, and F(ab)'2, F(ab)', Fab, Fv, scFv or V-min  
 CC humanized 55.1 constructs have been expressed in myeloma cells and E.  
 CC coli. (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SQ Sequence 239 AA;

Query Match 85.4%; Score 35; DB 2; Length 239;  
 Best Local Similarity 87.5%; Pred. No. 60;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8  
 |||||  
 Db 115 KOSYTLRT 122

RESULT 11  
 AA82743  
 ID AA82743 standard; protein; 288 AA.  
 XX  
 AC AA82743;  
 XX  
 DT 10-MAY-1999 (first entry)  
 XX  
 DE Fusion protein PNG4/55.1scFv/CPG2 R6/del ECORI.  
 XX  
 KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;  
 KW prodng-converting enzyme; cell surface antigen; treatment; cancer;

KW Inflammation; rheumatoid arthritis; antibody; produg therapy system.  
 XX Synthetic.  
 XX WO9851787-A2.  
 PN 19-NOV-1998.  
 PD 05-MAY-1998; 98WO-GB001294.  
 XX 10-MAY-1997; 97GB-00009421.  
 PR (ZENE ) ZENECA LTD.  
 XX Emery SC, Blakey DC;  
 PI WPI, 1999-059700/05.  
 XX N-PSDB; AAV72064.  
 DR New gene construct expressing conjugate of targeting agent and produg-  
 XX converting enzyme - useful for, e.g. targeted production of cytotoxic  
 PT drug in vivo, especially for treatment of cancer.  
 CC Example 15; Page 82; 100pp; English.  
 PS This sequence is a used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
 CC targeting group (I) and a heterologous produg-converting enzyme (II),  
 CC and (B) is directed to leave the cell for selective localisation at a  
 CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
 CC site, then administration of (II) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme produg therapy  
 CC system  
 CC Sequence 288 AA;  
 SQ

Query Match 85.4%; Score 35; DB 2; Length 288;  
 Best Local Similarity 87.5%; Pred. No. 72;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQSYNLT 8  
 Db 253 KQSYTLRT 260

RESULT 12  
 AAW82742  
 ID AAW82742 standard; protein; 673 AA.  
 XX AAW82742;  
 AC 10-MAY-1999 (first entry)  
 DT Plasmid pNG4/55.lscFv/CPG2 R6 protein.  
 XX  
 DE Conjugate; cell targeting; cytotoxic drug; produg-converting enzyme;  
 KW cell surface antigen; treatment; cancer; inflammation; antibody;  
 KW rheumatoid arthritis; produg therapy system.  
 XX Synthetic.  
 OS  
 XX WO9851787-A2.  
 PN 19-NOV-1998.  
 PD 05-MAY-1998; 98WO-GB001294.  
 PF 10-MAY-1997; 97GB-00009421.  
 XX (ZENE ) ZENECA LTD.  
 PA

XX Emery SC, Blakey DC;  
 PI WPI, 1999-059700/05.  
 DR N-PSDB; AAV72059.  
 XX New gene construct expressing conjugate of targeting agent and produg-  
 PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
 PT drug in vivo, especially for treatment of cancer.  
 CC Example 14; Page 78-79; 100pp; English.  
 PS This sequence is used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
 CC targeting group (I) and a heterologous produg-converting enzyme (II),  
 CC and (B) is directed to leave the cell for selective localisation at a  
 CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
 CC site, then administration of (II) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme produg therapy  
 CC system  
 CC Sequence 673 AA;  
 SQ

Query Match 85.4%; Score 35; DB 2; Length 673;  
 Best Local Similarity 87.5%; Pred. No. 1,7e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQSYNLT 8  
 Db 250 KQSYTLRT 257

RESULT 13  
 AAW60770  
 ID AAW60770 standard; protein; 249 AA.  
 XX AAW60770;  
 AC 08-SEP-1998 (first entry)  
 DT Single chain antibody (scFv) D3M that binds to mutant p53 proteins.  
 XX  
 DE Single chain antibody (scFv) D3M that binds to mutant p53 proteins.  
 KW regulatory domain; p53 mutant; H273; W248; G281;  
 KW p53-dependent trans-activating activity; restoration;  
 KW tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;  
 KW cancer; re-stenosis; ss.  
 XX Mus ap.  
 OS  
 XX WO9818825-A1.  
 PN 07-MAY-1998.  
 PD 27-OCT-1997; 97WO-FR001921.  
 PF 29-OCT-1996; 96FR-0001176.  
 XX (RHON ) RHONE-POULENC ROBER SA.  
 PA Bracco L, Debussche L;  
 PI WPI, 1998-272140/24.  
 DR N-PSDB; AAV36237.  
 XX Restoring p53-dependent trans-activating activity to cell containing  
 PT mutant p53 - by delivering single-chain antibody specific for the mutant,  
 PT particularly for treatment of tumours.  
 CC Claim 5; Page 32; 54pp; French.  
 PS

XX The present sequence represents a single chain antibody (ScFv) designated  
 CC D3M. The antibody binds to an epitope present in the C-terminal region of  
 CC the p53 protein that includes oligomerisation and regulatory domains,  
 CC specifically between positions 320 and 393. ScFv D3M is directed against  
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is  
 CC introduced into cells containing a mutant p53 protein, p53-dependent  
 CC trans-activating activity is restored. ScFv D3M is specific for p53-  
 CC mutants that have lost tumour-suppressing activity and are present in  
 CC tumour cells. It is particularly used to treat hyper-proliferation  
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
 CC and to purify or detect p53

XX Sequence 249 AA;

Query Match 82.9%; Score 34; DB 2; Length 249;  
 Best Local Similarity 87.5%; Pred. No. 1e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8  
 |||||  
 Db 232 KOSYNLPT 239

RESULT 14  
 AAW70910  
 ID AAW70910 standard; peptide; 8 AA.

XX AAW70910;  
 XX 14-OCT-1998 (first entry)  
 XX CDR3 of the light chain of monoclonal antibody RS-348.

XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
 KW respiratory syncytial virus; RSV; VP6 protein; roca virus; RV;  
 KW viral infection; inhibit; fusion; protection; transcription;  
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.

XX Synthetic.  
 OS Mus sp.

XX FR2758331-A1.  
 XX 17-JUL-1998.

XX 14-JAN-1997; 97FR-00000300.  
 XX 14-JAN-1997; 97FR-00000300.

XX (UYBO-) UNIV BOURGOGNE.  
 XX WPI; 1998-390320/34.

XX New peptide(s) recognising viral epitope with tropism to mucosa - useful  
 PT for, e.g. diagnosing, preventing and treating viral infection(s).

XX Claim 8; Fig 3; 51pp; French.

XX AAW70905-46 represent peptide sequences that can recognise, by antigen-  
 CC antibody type reactions, at least 1 epitope of a pathogenic virus having  
 CC tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR  
 CC regions of monoclonal antibodies specific for respiratory syncytial virus  
 CC (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies  
 CC specific for site III or IV of the VP6 protein of roca virus (RV). The  
 CC peptides can neutralise viral infections and may also inhibit fusion  
 CC between infected and uninfected cells or cells and viruses. They provide  
 CC passive or active protection and/or inhibit transcription of the virus,  
 CC so are useful as antiviral agents or for prophylaxis, in human or  
 CC veterinary medicine. The peptides can be labelled and used to diagnose  
 CC infection or contamination by the virus. The peptides are particularly  
 CC directed against RSV or RS but may also be used against papilloma, adeno,

CC entero, polio, influenza or immune deficiency viruses

XX Sequence 8 AA;

Query Match 80.5%; Score 33; DB 2; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+06;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8  
 |||||  
 Db 1 KOSYNLPT 8

RESULT 15  
 AAW70916  
 ID AAW70916 standard; peptide; 18 AA.

XX AAW70916;  
 XX 14-OCT-1998 (first entry)  
 XX Peptide PEP3L, homologous to light chain CDR3 of antibody RS-348.

XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;  
 KW respiratory syncytial virus; RSV; VP6 protein; roca virus; RV;  
 KW viral infection; inhibit; fusion; protection; transcription;  
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.

XX Synthetic.  
 OS Mus sp.

XX FR2758331-A1.  
 XX 17-JUL-1998.

XX 14-JAN-1997; 97FR-00000300.  
 XX 14-JAN-1997; 97FR-00000300.

XX (UYBO-) UNIV BOURGOGNE.  
 XX WPI; 1998-390320/34.

XX New peptide(s) recognising viral epitope with tropism to mucosa - useful  
 PT for, e.g. diagnosing, preventing and treating viral infection(s).

XX Claim 8; Fig 5; 51pp; French.

XX AAW70905-46 represent peptide sequences that can recognise, by antigen-  
 CC antibody type reactions, at least 1 epitope of a pathogenic virus having  
 CC tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR  
 CC regions of monoclonal antibodies specific for respiratory syncytial virus  
 CC (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies  
 CC specific for site III or IV of the VP6 protein of roca virus (RV). The  
 CC peptides can neutralise viral infections and may also inhibit fusion  
 CC between infected and uninfected cells or cells and viruses. They provide  
 CC passive or active protection and/or inhibit transcription of the virus,  
 CC so are useful as antiviral agents or for prophylaxis, in human or  
 CC veterinary medicine. The peptides can be labelled and used to diagnose  
 CC infection or contamination by the virus. The peptides are particularly  
 CC directed against RSV or RS but may also be used against papilloma, adeno,  
 CC entero, polio, influenza or immune deficiency viruses

XX Sequence 18 AA;

Query Match 80.5%; Score 33; DB 2; Length 18;  
 Best Local Similarity 87.5%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8  
 |||||  
 Db 4 KOSYNLPT 11

Search completed: March 1, 2005, 17:36:10  
Job time : 61.8154 secs



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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:39 ; Search time 15.6308 Seconds  
(without alignments)  
38.206 Million cell updates/sec

Title: US-10-071-962-20

Perfect score: 41

Sequence: 1 KOSYNLRT 8

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	114	3	US-08-929-856-66
2	41	100.0	265	2	US-08-403-853-16
3	36	87.8	109	2	US-08-308-494A-23
4	35	85.4	8	1	US-08-353-400-32
5	35	85.4	219	1	US-08-353-400-34
6	35	85.4	239	1	US-08-353-400-37
7	35	85.4	288	3	US-09-423-439-38
8	35	85.4	673	3	US-09-423-439-32
9	33	80.5	110	3	US-08-957-001B-5
10	33	80.5	110	3	US-08-957-001B-24
11	33	80.5	110	3	US-09-496-301-5
12	33	80.5	110	3	US-09-496-301-24
13	31	75.6	114	3	US-08-929-856-189
14	31	75.6	161	4	US-09-107-532A-5550
15	31	75.6	424	4	US-09-543-681A-7210
16	31	75.6	585	2	US-08-867-941-21
17	31	75.6	585	2	US-09-074-658-21
18	31	75.6	753	2	US-08-867-941-20
19	31	75.6	753	2	US-09-074-658-20
20	31	75.6	762	4	US-09-270-767-40204
21	31	75.6	762	4	US-09-270-767-55420
22	31	75.6	985	2	US-08-867-941-13
23	31	75.6	985	2	US-08-867-941-17
24	31	75.6	985	3	US-09-074-658-13
25	31	75.6	985	3	US-09-074-658-17
26	31	75.6	1000	2	US-08-867-941-12
27	31	75.6	1000	2	US-08-867-941-16

28	31	75.6	1000	3	US-09-074-658-12	Sequence 12, Appl
29	31	75.6	1000	3	US-09-074-658-16	Sequence 16, Appl
30	31	75.6	1003	4	US-09-540-236-3757	Sequence 2757, Ap
31	31	75.6	2432	3	US-09-074-658-15	Sequence 15, Appl
32	31	75.6	2439	3	US-09-074-658-11	Sequence 11, Appl
33	30	73.2	375	4	US-09-270-767-46302	Sequence 46302, A
34	30	73.2	401	4	US-09-270-767-56710	Sequence 56710, A
35	30	73.2	668	4	US-09-270-767-41490	Sequence 41490, A
36	30	73.2	754	4	US-09-976-594-375	Sequence 375, App
37	30	73.2	760	4	US-09-949-016-11129	Sequence 11129, A
38	29	70.7	8	4	US-09-627-896B-20	Sequence 20, Appl
39	29	70.7	117	4	US-09-149-476-642	Sequence 642, App
40	29	70.7	132	4	US-09-627-896B-4	Sequence 4, Appl
41	29	70.7	132	4	US-09-627-896B-8	Sequence 8, Appl
42	29	70.7	239	4	US-09-627-896B-22	Sequence 22, Appl
43	29	70.7	431	3	US-09-381-681-3	Sequence 3, Appl
44	29	70.7	441	3	US-09-191-136-31	Sequence 31, Appl
45	29	70.7	616	4	US-09-248-796A-24217	Sequence 24217, A

ALIGNMENTS

RESULT 1  
US-08-929-856-66  
Sequence 66, Application US/08929856  
Patent No. 6136568

GENERAL INFORMATION:  
Applicant: Hiatt, Andrew

Applicant: Rose, Floyd  
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING  
TITLE OF INVENTION: ROLLING TEMPLATES

NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &  
ADDRESS: MENTILIK  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA

ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

1	41	100.0	114	3	US-08-929-856-66	Sequence 66, Appl
2	41	100.0	265	2	US-08-403-853-16	Sequence 16, Appl
3	36	87.8	109	2	US-08-308-494A-23	Sequence 23, Appl
4	35	85.4	8	1	US-08-353-400-32	Sequence 32, Appl
5	35	85.4	219	1	US-08-353-400-34	Sequence 32, Appl
6	35	85.4	239	1	US-08-353-400-37	Sequence 37, Appl
7	35	85.4	288	3	US-09-423-439-38	Sequence 38, Appl
8	35	85.4	673	3	US-09-423-439-32	Sequence 32, Appl
9	33	80.5	110	3	US-08-957-001B-5	Sequence 5, Appl
10	33	80.5	110	3	US-08-957-001B-24	Sequence 24, Appl
11	33	80.5	110	3	US-09-496-301-5	Sequence 5, Appl
12	33	80.5	110	3	US-09-496-301-24	Sequence 24, Appl
13	31	75.6	114	3	US-08-929-856-189	Sequence 189, Appl
14	31	75.6	161	4	US-09-107-532A-5550	Sequence 5550, Ap
15	31	75.6	424	4	US-09-543-681A-7210	Sequence 7210, Ap
16	31	75.6	585	2	US-08-867-941-21	Sequence 21, Appl
17	31	75.6	585	2	US-09-074-658-21	Sequence 21, Appl
18	31	75.6	753	2	US-08-867-941-20	Sequence 20, Appl
19	31	75.6	753	2	US-09-074-658-20	Sequence 20, Appl
20	31	75.6	762	4	US-09-270-767-40204	Sequence 40204, A
21	31	75.6	762	4	US-09-270-767-55420	Sequence 55420, A
22	31	75.6	985	2	US-08-867-941-13	Sequence 13, Appl
23	31	75.6	985	2	US-08-867-941-17	Sequence 17, Appl
24	31	75.6	985	3	US-09-074-658-13	Sequence 13, Appl
25	31	75.6	985	3	US-09-074-658-17	Sequence 17, Appl
26	31	75.6	1000	2	US-08-867-941-12	Sequence 12, Appl
27	31	75.6	1000	2	US-08-867-941-16	Sequence 16, Appl

US-08-929-856-66

Query Match 100.0%; Score 41; DB 3; Length 114;  
Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 8; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8

DB 95 KOSYNLRT 102

RESULT 2  
US-08-403-853-16  
Sequence 16, Application US/08403853  
Patent No. 5844094  
GENERAL INFORMATION:  
APPLICANT: HUDSON, Peter J.  
APPLICANT: LAH, Maria  
APPLICANT: KORT, Alex A.  
APPLICANT: IRVING, Robert A.  
APPLICANT: ATWELL, John L.  
APPLICANT: MALBY, Robyn L.  
APPLICANT: POWER, Barbara E.  
APPLICANT: COLMAN, Peter M.  
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,853  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU93/00491  
FILING DATE: 24-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL 4973  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-403-853-16

Query Match 100.0%; Score 41; DB 2; Length 265;  
Best Local Similarity 100.0%; Pred. No. 0.37;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
Db 236 KOSYNLRT 243

RESULT 3  
US-08-308-494A-23  
Sequence 23, Application US/08308494A  
Patent No. 5959083  
GENERAL INFORMATION:  
APPLICANT: Bosselet, Klaus  
APPLICANT: Seesman, Gerhard  
TITLE OF INVENTION: Trivalent Bispecific Receptors, The  
TITLE OF INVENTION: Preparation and Use Thereof  
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,494A  
FILING DATE: 21-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/891,739  
FILING DATE: 01-JUN-1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4118120.4  
FILING DATE: 03-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kulik, David J.  
REGISTRATION NUMBER: 36,576  
REFERENCE/DOCKET NUMBER: 05552-1186-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-308-494A-23

Query Match 87.8%; Score 36; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLR 7  
Db 92 KOSYNLR 98

RESULT 4  
US-08-353-400-32  
Sequence 32, Application US/08353400  
Patent No. 5665357  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-32

Query Match 85.4%; Score 35; DB 1; Length 8;  
Best Local Similarity 87.5%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KOSYTLRT 8  
Db 1 KOSYTLRT 8

RESULT 5  
US-08-353-400-34  
Sequence 34, Application US/08353400  
Patent No. 5665357  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-34

Query Match 85.4%; Score 35; DB 1; Length 219;  
Best Local Similarity 87.5%; Pred. No. 6.2;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KOSYTLRT 8  
Db 95 KOSYTLRT 102

RESULT 6  
US-08-353-400-37  
Sequence 37, Application US/08353400  
Patent No. 5665357  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400

FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-37

Query Match 85.4%; Score 35; DB 1; Length 239;  
Best Local Similarity 87.5%; Pred. No. 6.8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KOSYTLRT 8  
Db 115 KOSYTLRT 122

RESULT 7  
US-09-423-439-38  
Sequence 38, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKLEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-423-439-38

Query Match 85.4%; Score 35; DB 3; Length 288;  
Best Local Similarity 87.5%; Pred. No. 8.3;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KOSYTLRT 8  
Db 253 KOSYTLRT 260

RESULT 8  
US-09-423-439-32  
Sequence 32, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-No. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-423-439-32  
Query Match 85.4%; Score 35; DB 3; Length 673;  
Best Local Similarity 87.5%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KOSYLT 8  
DB 250 KOSYLT 257  
RESULT 9  
US-08-957-001B-5  
Sequence 5, Application US/08957001B  
Patent No. 6228621  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madalo, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621r1s  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/957,001B  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
US-08-957-001B-5  
Query Match 80.5%; Score 33; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KOSYLT 8  
DB 95 KOSYLT 102  
RESULT 10  
US-08-957-001B-24  
Sequence 24, Application US/08957001B  
Patent No. 6228621  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madalo, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621r1s  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/957,001B  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-957-001B-24

Query Match 80.5%; Score 33; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
|||  
Db 95 KOSYLRRT 102

RESULT 11  
US-09-496-301-5  
Sequence 5, Application US/09496301  
Patent No. 6248565  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madaio, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565r1s  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
US-09-496-301-5

GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madaio, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565r1s  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-496-301-24

Query Match 80.5%; Score 33; DB 3; Length 110;  
Best Local Similarity 87.5%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
|||  
Db 95 KOSYLRRT 102

RESULT 13  
US-08-929-856-189  
Sequence 189, Application US/08929856  
Patent No. 6136568  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
APPLICANT: Rose, Floyd  
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLTZ &  
ADDRESS: MENTILIK  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/929,856  
FILING DATE: 15-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REGISTRATION NUMBER: 33,071  
REFERENCE/DOCKET NUMBER: ROSE 3.0-057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-929-856-189

Query Match 75.6%; Score 31; DB 3; Length 114;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYNLR 8  
Db 97 SYNLR 102

RESULT 14  
US-09-107-532A-5550  
Sequence 5550, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 5550:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES

ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1..161  
SEQUENCE DESCRIPTION: SEQ ID NO: 5550:  
US-09-107-532A-5550

Query Match 75.6%; Score 31; DB 4; Length 161;  
Best Local Similarity 62.5%; Pred. No. 33;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLR 8  
Db 145 EQYNI 152

RESULT 15  
US-09-543-681A-7210  
Sequence 7210, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709,1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 7210  
LENGTH: 424  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-7210

Query Match 75.6%; Score 31; DB 4; Length 424;  
Best Local Similarity 75.0%; Pred. No. 94;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQSYNLR 8  
Db 4 KTSYNLRS 11

Search completed: March 1, 2005, 17:46:58  
Job time: 16.6308 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:27:54 ; Search time 42.8308 Seconds  
(without alignments)  
61.273 Million cell updates/sec

Title: US-10-071-962-20

Perfect score: 41

Sequence: 1 KOSYNLRT 8

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 32804528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications MA:  
1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US09C\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	8	14 US-10-071-962-20	Sequence 20, Appl
2	33	80.5	542	16 US-10-437-963-119563	Sequence 119563,
3	32	78.0	318	9 US-09-971-536-66	Sequence 66, Appl
4	32	78.0	453	17 US-10-706-635-14	Sequence 14, Appl
5	31	75.6	422	15 US-10-282-122A-69060	Sequence 69060, A
6	31	75.6	541	15 US-10-398-570-3	Sequence 3, Appl1
7	31	75.6	546	14 US-10-091-007-2	Sequence 2, Appl1
8	30	73.2	61	16 US-10-437-963-152957	Sequence 152957,
9	30	73.2	115	16 US-10-767-701-38209	Sequence 38209, A
10	30	73.2	126	11 US-09-864-408A-4176	Sequence 4176, Ap
11	30	73.2	235	16 US-10-437-963-145300	Sequence 145300,
12	30	73.2	237	17 US-10-472-928-1306	Sequence 1306, Ap
13	30	73.2	251	15 US-10-424-599-211909	Sequence 211909,

14	30	73.2	330	13 US-10-058-566-2	Sequence 2, Appl1
15	30	73.2	330	16 US-10-437-963-142973	Sequence 142973,
16	30	73.2	428	15 US-10-425-114-50411	Sequence 50411, A
17	30	73.2	448	14 US-10-153-668-370	Sequence 370, App
18	30	73.2	683	16 US-10-620-669-20	Sequence 20, Appl
19	30	73.2	737	16 US-10-620-669-18	Sequence 18, Appl
20	30	73.2	754	14 US-10-153-668-254	Sequence 254, App
21	30	73.2	1720	16 US-10-437-963-114206	Sequence 114206,
22	29	70.7	8	9 US-09-249-011A-2	Sequence 20, Appl
23	29	70.7	83	15 US-10-424-599-157776	Sequence 157776,
24	29	70.7	117	10 US-09-809-391-642	Sequence 642, App
25	29	70.7	117	10 US-09-882-171-642	Sequence 642, App
26	29	70.7	117	15 US-10-164-861-642	Sequence 642, App
27	29	70.7	122	16 US-10-767-701-39825	Sequence 39825, A
28	29	70.7	132	9 US-09-249-011A-4	Sequence 4, Appl1
29	29	70.7	132	9 US-09-249-011A-8	Sequence 4, Appl1
30	29	70.7	239	9 US-09-249-011A-22	Sequence 22, Appl
31	29	70.7	302	15 US-10-425-114-46501	Sequence 46501, A
32	29	70.7	380	15 US-10-282-122A-54278	Sequence 54278, A
33	29	70.7	405	10 US-09-820-095-2	Sequence 2, Appl1
34	29	70.7	429	15 US-10-282-122A-78300	Sequence 78300, A
35	29	70.7	431	10 US-09-820-095-4	Sequence 4, Appl1
36	29	70.7	434	10 US-09-981-151A-66	Sequence 66, Appl
37	29	70.7	531	13 US-10-408-765A-1597	Sequence 1597, Ap
38	29	70.7	531	13 US-10-047-260-32	Sequence 32, Appl
39	29	70.7	547	10 US-09-977-418-4	Sequence 4, Appl1
40	29	70.7	547	10 US-09-977-033A-4	Sequence 4, Appl1
41	29	70.7	547	10 US-09-977-751C-4	Sequence 4, Appl1
42	29	70.7	547	10 US-09-977-639A-4	Sequence 4, Appl1
43	29	70.7	547	10 US-09-981-151A-24	Sequence 24, Appl
44	29	70.7	547	11 US-09-977-819B-4	Sequence 4, Appl1
45	29	70.7	548	15 US-10-425-114-67811	Sequence 67811, A

#### ALIGNMENTS

RESULT 1  
US-10-071-962-20  
Sequence 20, Application US/10071962  
Publication No. US20030170237A1  
GENERAL INFORMATION:  
APPLICANT: Baitu Ni  
APPLICANT: Bill N.C. Sun  
TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and  
FILE REFERENCE: 98-3  
CURRENT APPLICATION NUMBER: US/10/071,962  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US/09/303,155A  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: 60/083,575  
PRIOR FILING DATE: 1998-04-30  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 8  
TYPE: PRT  
ORGANISM: mouse  
US-10-071-962-20

Query Match  
Best local similarity  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 KOSYNLRT 8  
Db 1 KOSYNLRT 8

RESULT 2  
US-10-437-963-119563

/ Sequence 119563, Application US/10437963  
/ Publication No. US20040123343A1  
/ GENERAL INFORMATION:  
/ APPLICANT: La Rosa, Thomas J.  
/ APPLICANT: Kovalic, David K.  
/ APPLICANT: Zhou, Yihua  
/ APPLICANT: Cao, Yongwei  
/ APPLICANT: Wu, Wei  
/ APPLICANT: Boukharov, Andrey A.  
/ APPLICANT: Barbazuk, Brad  
/ APPLICANT: Li, Ping  
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
/ FILE REFERENCE: 38-21(53221)B  
/ CURRENT APPLICATION NUMBER: US/10/437,963  
/ CURRENT FILING DATE: 2003-05-14  
/ NUMBER OF SEQ ID NOS: 204966  
/ SEQ ID NO 119563  
/ LENGTH: 542  
/ TYPE: PRT  
/ ORGANISM: Oryza sativa  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: PAT\_MRT4530\_22769C.1.pep  
/ US-10-437-963-119563

Query Match 80.5%; Score 33; DB 16; Length 542;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLR 7  
DB 457 KOSYNLR 463

RESULT 3  
/ US-09-971-536-66  
/ Sequence 66, Application US/0971536  
/ Patent No. US20020159976A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Glenn, Matthew  
/ APPLICANT: Havukkala, Ilkka  
/ APPLICANT: Bloksberg, Leonard  
/ APPLICANT: Lubbers, Mark  
/ APPLICANT: Dekker, James  
/ APPLICANT: Christenson, Anna  
/ APPLICANT: Holland, Rose  
/ APPLICANT: O'Toole, Paul  
/ APPLICANT: Reid, Julian  
/ APPLICANT: Coolbear, Timothy  
/ TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Methods  
/ TITLE OF INVENTION: Using Them  
/ FILE REFERENCE: 104362  
/ CURRENT APPLICATION NUMBER: US/09/971,536  
/ CURRENT FILING DATE: 2001-10-02  
/ PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238  
/ PRIOR FILING DATE: 2000-08-08  
/ PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623  
/ PRIOR FILING DATE: 2000-11-28  
/ PRIOR APPLICATION NUMBER: PCT/NZ01/00160  
/ PRIOR FILING DATE: 2001-08-08  
/ NUMBER OF SEQ ID NOS: 83  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 66  
/ LENGTH: 318  
/ TYPE: PRT  
/ ORGANISM: Lactobacillus rhamnosus  
/ US-09-971-536-66

Query Match 78.0%; Score 32; DB 9; Length 318;  
Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLR 7

DB 73 KOSYNLR 79

RESULT 4  
/ US-10-706-635-14  
/ Sequence 14, Application US/10706635  
/ Publication No. US20050014263A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Moyer, Richard W.  
/ APPLICANT: Li, Yi  
/ TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous  
/ TITLE OF INVENTION: Vertebrate Cells  
/ FILE REFERENCE: UF-221C1XC21  
/ CURRENT APPLICATION NUMBER: US/10/706,635  
/ CURRENT FILING DATE: 2003-11-12  
/ PRIOR APPLICATION NUMBER: 09/086,651  
/ PRIOR FILING DATE: 1998-05-29  
/ PRIOR APPLICATION NUMBER: 09/662,254  
/ PRIOR FILING DATE: 2000-09-14  
/ PRIOR APPLICATION NUMBER: 60/224,479  
/ PRIOR FILING DATE: 2000-08-10  
/ NUMBER OF SEQ ID NOS: 80  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 14  
/ LENGTH: 453  
/ TYPE: PRT  
/ ORGANISM: Ambaceta moorei entomopoxvirus  
/ US-10-706-635-14

Query Match 78.0%; Score 32; DB 17; Length 453;  
Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOSYNLR 8  
DB 156 KOSYNLR 163

RESULT 5  
/ US-10-282-122A-69060  
/ Sequence 69060, Application US/10282122A  
/ Publication No. US20040029129A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Wang, Lianguu  
/ APPLICANT: Zamudio, Carlos  
/ APPLICANT: Malone, Cheryl  
/ APPLICANT: Haselbeck, Robert  
/ APPLICANT: Ohlsen, Karl  
/ APPLICANT: Zyskind, Judith  
/ APPLICANT: Wall, Daniel  
/ APPLICANT: Trawick, John  
/ APPLICANT: Carr, Grant  
/ APPLICANT: Yamamoto, Robert  
/ APPLICANT: Foreyth, R.  
/ APPLICANT: Xu, H.  
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
/ FILE REFERENCE: ELITRA.034A  
/ CURRENT APPLICATION NUMBER: US/10/282,122A  
/ CURRENT FILING DATE: 2003-02-20  
/ PRIOR APPLICATION NUMBER: 60/191,078  
/ PRIOR FILING DATE: 2000-03-21  
/ PRIOR APPLICATION NUMBER: 60/206,848  
/ PRIOR FILING DATE: 2000-05-23  
/ PRIOR APPLICATION NUMBER: 60/207,727  
/ PRIOR FILING DATE: 2000-05-26  
/ PRIOR APPLICATION NUMBER: 60/230,335  
/ PRIOR FILING DATE: 2000-09-06  
/ PRIOR APPLICATION NUMBER: 60/230,347  
/ PRIOR FILING DATE: 2000-09-09  
/ PRIOR APPLICATION NUMBER: 60/242,578  
/ PRIOR FILING DATE: 2000-10-23  
/ PRIOR APPLICATION NUMBER: 60/253,625



;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/267,636  
;; PRIOR FILING DATE: 2001-02-09  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 78614  
;; SOFTWARE: Patent version 3.1  
;; SEQ ID NO 69060  
;; LENGTH: 422  
;; TYPE: PRT  
;; ORGANISM: Proteus mirabilis  
US-10-282-122A-69060

Query Match 75.6%; Score 31; DB 15; Length 422;  
Best Local Similarity 75.0%; Pred. No. 4e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KOSYNLR 8  
Db 2 KTSYNLRS 9

RESULT 6  
US-10-398-570-3  
;; Sequence 3, Application US/10398570  
;; Publication No. US20040071730A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SHIRE BIOCHEM INC.  
;; APPLICANT: MARTIN, Denis  
;; APPLICANT: BOYER, Stephane  
;; APPLICANT: RIOUX, Martine  
;; APPLICANT: HAMEL, Josee  
;; APPLICANT: BRODEUR, Bernard R.  
;; TITLE OF INVENTION: BVH-A2 and BVH-A3 ANTIGENS OF GBS  
;; FILE REFERENCE: 12806-23PCT  
;; CURRENT APPLICATION NUMBER: US/10/398,570  
;; CURRENT FILING DATE: 2003-04-08  
;; PRIOR APPLICATION NUMBER: US 60/239,919  
;; PRIOR FILING DATE: 2000-10-13  
;; NUMBER OF SEQ ID NOS: 21  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 541  
;; TYPE: PRT  
;; ORGANISM: Group B Streptococcus  
US-10-398-570-3

Query Match 75.6%; Score 31; DB 15; Length 541;  
Best Local Similarity 85.7%; Pred. No. 5.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOSYNLR 7  
Db 8 KQSYSLR 14

RESULT 7  
US-10-091-007-2  
;; Sequence 2, Application US/10091007  
;; Publication No. US20030170782A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Microbial Technics limited  
;; APPLICANT: Le Page, Richard W P Wells, Jeremy M  
;; APPLICANT: Hamifly, Sean B  
;; TITLE OF INVENTION: Proteins  
;; FILE REFERENCE: PWC/P21978MO  
;; CURRENT APPLICATION NUMBER: US/10/091,007  
;; CURRENT FILING DATE: 2002-03-06  
;; PRIOR APPLICATION NUMBER: GB 9921125.2  
;; PRIOR FILING DATE: 1999-09-07

;; NUMBER OF SEQ ID NOS: 276  
;; SOFTWARE: Patent version 3.0  
;; SEQ ID NO 2  
;; LENGTH: 546  
;; TYPE: PRT  
;; ORGANISM: Streptococcus agalactiae  
US-10-091-007-2

Query Match 75.6%; Score 31; DB 14; Length 546;  
Best Local Similarity 85.7%; Pred. No. 5.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOSYNLR 7  
Db 13 KQSYSLR 19

RESULT 8  
US-10-437-963-152957  
;; Sequence 152957, Application US/10437963  
;; Publication No. US20040123343A1  
;; GENERAL INFORMATION:  
;; APPLICANT: La Rosa, Thomas J.  
;; APPLICANT: Kovalic, David K.  
;; APPLICANT: Zhou, Yihua  
;; APPLICANT: Cao, Yongwei  
;; APPLICANT: Wu, Wei  
;; APPLICANT: Boukharov, Andrey A.  
;; APPLICANT: Barbazuk, Brad  
;; APPLICANT: Li, Ping  
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
;; FILE REFERENCE: 38-21(53221)B  
;; CURRENT APPLICATION NUMBER: US/10/437,963  
;; CURRENT FILING DATE: 2003-05-14  
;; NUMBER OF SEQ ID NOS: 204966  
;; SEQ ID NO 152957  
;; LENGTH: 61  
;; TYPE: PRT  
;; ORGANISM: Oryza sativa  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_52957C.1.pep  
US-10-437-963-152957

Query Match 73.2%; Score 30; DB 16; Length 61;  
Best Local Similarity 85.7%; Pred. No. 90;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 OSYNLRT 8  
Db 4 QSYRLRT 10

RESULT 9  
US-10-767-701-38209  
;; Sequence 38209, Application US/10767701  
;; Publication No. US20040172684A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Kovalic, David K.  
;; APPLICANT: Zhou, Yihua  
;; APPLICANT: Cao, Yongwei  
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
;; FILE REFERENCE: 38-21(53535)B  
;; CURRENT APPLICATION NUMBER: US/10/767,701  
;; CURRENT FILING DATE: 2004-01-29  
;; NUMBER OF SEQ ID NOS: 63128  
;; SEQ ID NO 38209  
;; LENGTH: 115  
;; TYPE: PRT  
;; ORGANISM: Sorghum bicolor  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C50410\_1.pep

US-10-767-701-38209

## Query Match

Best Local Similarity 73.2%; Score 30; DB 16; Length 115;  
 Pred. No. 1,7e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
 |||||  
 DB 73 KOSYQLNT 80

## RESULT 10

US-09-864-408A-4176  
 ; Sequence 4176, Application US/09864408A  
 ; Publication No. US2004009474A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leach, Martin D.  
 ; APPLICANT: Shimkets, Richard A.  
 ; TITLE OF INVENTION: No. US2004009474A1 Human Polynucleotides and Polypeptides Encc  
 ; FILE REFERENCE: 21402-012  
 ; CURRENT APPLICATION NUMBER: US/09/864,408A  
 ; CURRENT FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: 60/206,690  
 ; PRIOR FILING DATE: 2000-05-24  
 ; NUMBER OF SEQ ID NOS: 9068  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4176  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-864-408A-4176

## Query Match

Best Local Similarity 73.2%; Score 30; DB 11; Length 126;  
 Pred. No. 1,9e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
 |||||  
 DB 92 KOSYQLNT 99

## RESULT 11

US-10-437-963-145300  
 ; Sequence 145300, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barzduk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 145300  
 ; LENGTH: 235  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_46032C.1.pep  
 ; US-10-437-963-145300

## Query Match

Best Local Similarity 73.2%; Score 30; DB 16; Length 235;  
 Pred. No. 3,5e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8

DB 224 KOSYNLRT 231  
 |||||

## RESULT 12

US-10-472-928-1306  
 ; Sequence 1306, Application US/10472928  
 ; Publication No. US20050020813A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SpA  
 ; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH  
 ; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE: P026926W0  
 ; CURRENT APPLICATION NUMBER: US/10/472,928  
 ; CURRENT FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: GB-0107658.7  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 4979  
 ; SOFTWARE: SeqWin99, version 1.03  
 ; SEQ ID NO 1306  
 ; LENGTH: 237  
 ; TYPE: PRT  
 ; ORGANISM: Streptococcus pneumoniae  
 ; FEATURE:  
 ; OTHER INFORMATION: hypothetical protein  
 ; OTHER INFORMATION: Cellular location: membrane  
 ; OTHER INFORMATION: Similar to strain R6 sequence 15902655 (e-127)  
 ; US-10-472-928-1306

## Query Match

Best Local Similarity 73.2%; Score 30; DB 17; Length 237;  
 Pred. No. 3,6e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
 |||||  
 DB 79 KEXNLQT 86

## RESULT 13

US-10-424-599-211909  
 ; Sequence 211909, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 211909  
 ; LENGTH: 251  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_33380C.1.pep  
 ; US-10-424-599-211909

## Query Match

Best Local Similarity 73.2%; Score 30; DB 15; Length 251;  
 Pred. No. 3,8e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 7  
 |||||  
 DB 206 KOSYQLRT 212

## RESULT 14

US-10-058-566-2  
 ; Sequence 2, Application US/10058566

; Publication No. US20020183274A1  
; GENERAL INFORMATION:  
; APPLICANT: ALBERTSEN, MARC  
; APPLICANT: FOX, TIM  
; APPLICANT: HUFFMAN, GARY  
; APPLICANT: TRIMNELL, MARY  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND  
; FILE REFERENCE: PRT 1147  
; CURRENT APPLICATION NUMBER: US/10/058,566  
; CURRENT FILING DATE: 2002-01-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 2  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-058-566-2

Query Match 73.2%; Score 30; DB 13; Length 330;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KOSYNLRT 8  
|||  
Db 288 KOSYELNT 295

RESULT 15  
US-10-437-963-142973  
; Sequence 142973, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO: 142973  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_43928C.1.pap  
US-10-437-963-142973

Query Match 73.2%; Score 30; DB 16; Length 330;  
Best Local Similarity 75.0%; Pred. No. 5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KOSYNLRT 8  
|||  
Db 288 KOSYELNT 295

Search completed: March 1, 2005, 17:52:52  
Job time : 43.8308 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 17:25:09 ; Search time 10.8308 Seconds  
(without alignments)  
71.065 Million cell updates/sec

Title: US-10-071-962-20

Perfect score: 41

Sequence: 1 KOSYNLRT 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	103	2 PH1050	Ig light chain V r
2	41	100.0	104	2 PH1101	Ig light chain V r
3	41	100.0	104	2 PH1102	Ig light chain V r
4	41	100.0	112	2 S41393	Ig kappa chain V r
5	41	100.0	112	2 S41303	Ig kappa chain V-J
6	41	100.0	133	2 P60023	Ig kappa chain pre
7	34	82.9	97	2 A42575	Ig kappa chain V r
8	34	82.9	103	2 PH1047	Ig light chain V r
9	34	82.9	103	2 PH1051	Ig light chain V r
10	34	82.9	103	2 PH1052	Ig light chain V r
11	34	82.9	104	2 PH1103	Ig light chain V r
12	34	82.9	113	2 P70408	Ig light chain V r
13	34	82.9	113	2 P70407	Ig light chain V r
14	32	78.0	50	2 F97819	Ig light chain V r
15	32	78.0	2	SS3840	hypothetical prote
16	31	75.6	120	2 G33932	hypothetical prote
17	31	75.6	549	2 H96944	Ig kappa chain pre
18	31	75.6	566	2 S39732	arginine degradati
19	31	75.6	667	2 C87236	arginine/ornithine
20	31	75.6	761	1 S52769	probable zinc meta
21	30	73.2	104	2 PH1104	subtilisin-like pr
22	30	73.2	173	2 A70133	Ig light chain V r
23	30	73.2	237	2 A95081	hypothetical prote
24	30	73.2	237	2 C97948	hypothetical prote
25	30	73.2	392	2 H81408	probable periplasm
26	30	73.2	520	2 J50291	intermediate filam
27	30	73.2	717	2 S78177	hypothetical prote
28	30	73.2	754	1 JCS314	CDC28/cdc2-like ki
29	30	73.2	770	2 S75042	hypothetical prote

30	30	73.2	859	1 S06418	3',5'-cyclic-GMP p
31	30	73.2	2244	2 P90563	hypothetical prote
32	30	73.2	3724	2 T18427	hypothetical prote
33	29	70.7	133	2 A41328	hypothetical prote
34	29	70.7	197	2 T38418	probable coiled-co
35	29	70.7	212	2 P97033	probable membrane-
36	29	70.7	231	2 A11262	ABC transporter, A
37	29	70.7	231	2 A11625	ABC transporter, A
38	29	70.7	234	2 U70874	purine-nucleoside
39	29	70.7	346	2 H72237	hypothetical prote
40	29	70.7	352	2 T51935	ribosomal protein
41	29	70.7	380	2 P81449	8-amino-7-oxonon
42	29	70.7	421	2 E69467	hypothetical prote
43	29	70.7	429	2 A10029	conserved hypothet
44	29	70.7	522	2 AD2344	hypothetical prote
45	29	70.7	524	2 S07168	probable maturase,

#### ALIGNMENTS

##### RESULT 1

PH1050  
Ig light chain V region (clone 111-cl) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1050

R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and IGC anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; PMID:92381444; PMID:1512540

A:Accession: PH1050

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-103 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.077;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KOSYNLRT 8  
Db 95 KOSYNLRT 102

##### RESULT 2

PH1101  
Ig light chain V region (clone 111.19) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1101

R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and IGC anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; PMID:92381444; PMID:1512540

A:Accession: PH1101

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-104 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 0.078;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KOSYNLRT 8

Db 95 KOSYNLRT 102

## RESULT 3

PH1102  
Ig light chain V region (clone 111.61) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C/Accession: PH1102  
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A/Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c  
A/Reference number: PH0971; PMID:92361444; PMID:1512540  
A/Accession: PH1102  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-104 <TIL>  
A/Experimental source: B cell, strain [NZB x NZW]F1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOSYNLRT 8  
Db 95 KOSYNLRT 102

## RESULT 4

S41393  
Ig kappa chain V region (12.5H VL) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-2001  
C/Accession: S41393  
R/Margarte, C.; Gilbert, D.; Brard, F.; Tron, F.  
submitted to the EMBL Data Library, January 1994  
A/Description: Structural characterization of an (NZB x NZW)F1 mouse-derived IGM anti-DN  
A/Reference number: S41393  
A/Accession: S41393  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-112 <MAR>  
A/Cross-references: EMBL:Z29536  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOSYNLRT 8  
Db 95 KOSYNLRT 102

## RESULT 5

S43103  
Ig kappa chain V-J region (4B1 VL) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 24-May-2001  
C/Accession: S43103  
R/Gilbert, D.; Brard, F.; Margarte, C.; Delpech, A.; Tron, F.  
submitted to the EMBL Data Library, March 1994  
A/Description: An idiotype D23-bearing polyclonal antibody  
A/Reference number: S42484  
A/Accession: S43103  
A/Status: preliminary  
A/Molecule type: mRNA

A/Residues: 1-112 <GIL>  
A/Cross-references: EMBL:Z21353; NID:G467574; PIDN:CAA83231.1; PID:G467575  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOSYNLRT 8  
Db 95 KOSYNLRT 102

## RESULT 6

PS0023  
Ig kappa chain precursor V region (6A4) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C/Accession: PS0023  
R/Margat, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Dondey, H.  
Gene 74, 335-345, 1988  
A/Title: Cloning and characterization of cDNAs coding for the heavy and light chains of e  
A/Reference number: PS0023; PMID:89232725; PMID:3149944  
A/Accession: PS0023  
A/Molecule type: mRNA  
A/Residues: 1-133 <MAR>  
A/Experimental source: strain BALB/c  
A/Note: the amino-terminal four residues of the mature protein were directly sequenced  
C/Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aerugin  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>  
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 41; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOSYNLRT 8  
Db 115 KOSYNLRT 122

## RESULT 7

A42575  
Ig kappa chain V region (anti-angiotensin II) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C/Accession: A42575  
R/Garcia, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M.  
Science 257, 528-531, 1992  
A/Title: Recognition of angiotensin II: antibodies at different levels of an idiotypic n  
A/Reference number: A42575; PMID:92342952; PMID:1636087  
A/Accession: A42575  
A/Molecule type: mRNA  
A/Residues: 1-97 <GAR>  
A/Cross-references: GB:S40673; NID:G252096; PIN:AA822668.1; PID:G252097  
A/Experimental source: BALB/c mice, myeloma cell line NS-1  
C/Note: sequence extracted from NCBI backbone (NCBIN:109331, NCBI:P.109336)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F:8-68/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 34; DB 2; Length 97;  
Best Local Similarity 87.5%; Pred. No. 2.6;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KOSYNLRT 8  
Db 87 KOSYNLRT 94

## RESULT 8

PH1047

Ig light chain V region (clones 165.45 and 163-cl) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1047; PH1049

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1047

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-103 &lt;TIL&gt;

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 103;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8

Db 95 KOSYNLRT 102

## RESULT 9

PH1051

Ig light chain V region (clone 165.3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1051

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1051

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-103 &lt;TIL&gt;

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 103;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8

Db 95 KOSYNLRT 102

## RESULT 10

PH1052

Ig light chain V region (clone 165.5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1052

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1052

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-103 &lt;TIL&gt;

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

## Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 103;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8

Db 95 KOSYNLRT 102

## RESULT 11

PH1103

Ig light chain V region (clone 111.109) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1103

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1103

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-104 &lt;TIL&gt;

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 104;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8

Db 95 KOSYNLRT 102

## RESULT 12

PT0408

Ig light chain V region (S107/VH11 group 1-6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PT0408

R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.

J. Exp. Med. 173, 731-741, 1991

A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi

A:Reference number: PT0376; MUID:91147903; PMID:1900082

A:Accession: PT0408

A:Residues: 1-113 &lt;BEH&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-96/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 113;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOSYNLRT 8

Db 95 KOSYNLRT 102

## RESULT 13

PT0407

Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PT0407

R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.  
J. Exp. Med. 173, 731-741, 1991  
A>Title: Characterization of somatically mutated SI07 VH11-encoded anti-DNA autoantibody  
A:Reference number: PT0376; MUID:2147903; PMID:1900082  
A/Accession: PT0407  
A/Molecule type: DNA  
A:Residues: 1-113 <BEH>  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 34; DB 2; Length 113;  
Best Local Similarity 87.5%; Pred. No. 3.1;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
DB 95 KOSYNLRT 102

## RESULT 14

F97819  
hypothetical protein RC0958 [imported] - Rickettsia conorii (strain Malish 7)

C/Species: Rickettsia conorii  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: F97819

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rickettsia conorii and Rickettsia prowazekii.  
Science 293, 2093-2098, 2001

A/Reference number: A97700; MUID:21442074; PMID:11557893

A/Accession: F97819

A/Status: preliminary

A/Molecule type: DNA

A:Residues: 1-50 <KUR>

A/Cross-references: UNIPROT:Q92H14; GB:AB006914; PIDN:AAL03496.1; PID:G15620070; GSPDB:G

C/Genetics: RC0958

Query Match 78.0%; Score 32; DB 2; Length 50;  
Best Local Similarity 85.7%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLR 7  
DB 37 KOSYNLR 43

## RESULT 15

S53840  
hypothetical protein 83 - Acanthamoeba castellanii mitochondrion

C/Species: mitochondrion Acanthamoeba castellanii  
C/Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004

C/Accession: S53840

R:Burger, G.; Planete, I.; Loneragan, K.M.; Gray, M.W.  
J. Mol. Biol. 245, 522-537, 1995

A/Title: The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba castellanii: complete sequence  
A/Reference number: S53825; MUID:55147275; PMID:7844823

A/Accession: S53840

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A:Residues: 1-83 <BUR>

A/Cross-references: UNIPROT:Q03664; GB:U12386; NID:G562028; PIDN:AAD11832.1; PID:G562044

A/Experimental source: strain Neff, ATCC 30010

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

C/Genetics:

A/Genome: mitochondrion

A/genetic code: SGC6

C/Keywords: mitochondrion

Query Match 78.0%; Score 32; DB 2; Length 83;  
Best Local Similarity 62.5%; Pred. No. 6.1;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLRT 8  
DB 12 KOSFNIRT 19

Search completed: March 1, 2005, 17:44:47  
Job time: 11.8308 secs





Q9GHC8  
ID Q9GHC8 PRELIMINARY; PRT; 515 AA.  
AC Q9GHC8;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Helionopsis umbellata;  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=120002;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040195; BAB16803.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; Matk\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; Matk\_N; 1.  
KM Chloroplast.  
SQ SEQUENCE 515 AA; 61977 MW; BA896191DB66FDF6 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KOSYNLR 7  
Db 234 KOSYNLR 240

RESULT 3  
Q9GHC9  
ID Q9GHC9 PRELIMINARY; PRT; 515 AA.  
AC Q9GHC9;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Helionopsis orientalis;  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040194; BAB16802.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; Matk\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; Matk\_N; 1.  
KM Chloroplast.  
SQ SEQUENCE 515 AA; 61852 MW; 2B33690D42B60290 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;

Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KOSYNLR 7  
Db 234 KOSYNLR 240

RESULT 4  
Q9GHD0  
ID Q9GHD0 PRELIMINARY; PRT; 515 AA.  
AC Q9GHD0;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Helionopsis orientalis;  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040193; BAB16801.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron\_maturase2.  
DR InterPro; IPR002866; Matk\_N.  
DR Pfam; PF01348; Intron\_maturase2; 1.  
DR Pfam; PF01824; Matk\_N; 1.  
KM Chloroplast.  
SQ SEQUENCE 515 AA; 61844 MW; 1BBFF413F5DE7848 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 515;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KOSYNLR 7  
Db 234 KOSYNLR 240

RESULT 5  
Q9GHD1  
ID Q9GHD1 PRELIMINARY; PRT; 515 AA.  
AC Q9GHD1;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Helionopsis orientalis;  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthiaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040192; BAB16800.1; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.

DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron mature2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_mature2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61747 MW; 66A8A1DDA39BFB CRC64;

Query Match  
Best Local Similarity 87.8%; Score 36; DB 2; Length 515;  
Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOSYNLR 7  
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|||  
Db 234 KOSYNLR 240

RESULT 6  
Q9GHD2 PRELIMINARY; PRT; 515 AA.  
ID Q9GHD2  
AC Q9GHD2;

DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Helionopsis orientalis.

OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040191; BAB16799.1; -.

DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron mature2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_mature2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.

SQ SEQUENCE 515 AA; 61780 MW; A4932FD7A8600BA8 CRC64;  
Query Match  
Best Local Similarity 87.8%; Score 36; DB 2; Length 515;  
Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOSYNLR 7  
|||  
|||  
Db 234 KOSYNLR 240

RESULT 7  
Q9GHD3 PRELIMINARY; PRT; 515 AA.  
ID Q9GHD3  
AC Q9GHD3;

DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Helionopsis orientalis.

OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040190; BAB16798.2; -.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron mature2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_mature2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.  
SQ SEQUENCE 515 AA; 61923 MW; 898AAB45F7477E9F CRC64;

Query Match  
Best Local Similarity 87.8%; Score 36; DB 2; Length 515;  
Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOSYNLR 7  
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|||  
Db 234 KOSYNLR 240

RESULT 8  
Q9GHD4 PRELIMINARY; PRT; 515 AA.  
ID Q9GHD4  
AC Q9GHD4;

DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Maturase.  
GN Name=matk;  
OS Helionopsis orientalis.

OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Fuse S., Tamura M.N.;  
RT "A phylogenetic analysis of the plastid matk gene with emphasis on  
RT Melanthaceae sensu lato."  
RL Plant Biol. 2:415-427(2000).  
DR EMBL; AB040189; BAB16797.2; -.

DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0008380; P:RNA splicing; IEA.  
DR InterPro; IPR008998; Agglutinin.  
DR InterPro; IPR000442; Intron mature2.  
DR InterPro; IPR002866; MatK\_N.  
DR Pfam; PF01348; Intron\_mature2; 1.  
DR Pfam; PF01824; MatK\_N; 1.  
KW Chloroplast.

SQ SEQUENCE 515 AA; 61834 MW; 590865E229969D6 CRC64;  
Query Match  
Best Local Similarity 87.8%; Score 36; DB 2; Length 515;  
Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOSYNLR 7  
|||  
|||  
Db 234 KOSYNLR 240

RESULT 9  
Q9GHD5 PRELIMINARY; PRT; 515 AA.  
ID Q9GHD5  
AC Q9GHD5;

DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthaceae;  
OC Helionopsis.  
OX NCBI\_TaxID=87628;



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us-10-071-962-20.rup

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KW Chloroplast.
SQ SEQUENCE 515 AA; 61796 MW; 1C8FF71CA6CEP8 CRC64;

Query Match
Best Local Similarity 87.8%; Score 36; DB 2; Length 515;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLR 7
   |||||
Db 234 KOSYNLR 240

RESULT 13
QYJUL7 PRELIMINARY; PRT; 521 AA.
ID QYJUL7
AC QYJUL7;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Maturase.
GN Name=matk;
OS Chortolirion angolense.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asphodelaceae;
OC Chortolirion.
OX NCBI_TaxID=210957;
RN [1]
RP SEQUENCE FROM N.A.
RA Treutlein J., Smith G.F., van Wyk B.-E., Wink M.;
RT "Phylogenetic relationships in Asphodelaceae (subfamily Allooideae)
RT inferred from chloroplast DNA sequences (rbcL, matk) and from genomic
RT fingerprinting (ISSR).";
RL Taxon 52:193-207(2003).
DR EMBL; AJ511393; CAD54537.1; -.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR008998; Agglutinin.
DR InterPro; IPR000442; Intron_mature2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_mature2; 1.
DR Pfam; PF01824; MatK_N; 1.
DR PIRam; PIR002866; MatK_N.
SQ SEQUENCE 521 AA; 62846 MW; 8841EAA964DA0343 CRC64;

Query Match
Best Local Similarity 87.8%; Score 36; DB 2; Length 521;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLR 7
   |||||
Db 235 KOSYNLR 241

RESULT 14
QYJUL7 PRELIMINARY; PRT; 521 AA.
ID QYJUL7
AC QYJUL7;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Maturase.
GN Name=matk;
OS Aloe ramosissima.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asphodelaceae;
OC Aloe.
OX NCBI_TaxID=210944;
RN [1]
RP SEQUENCE FROM N.A.
RA Treutlein J., Smith G.F., van Wyk B.-E., Wink M.;
RT "Phylogenetic relationships in Asphodelaceae (subfamily Allooideae)
RT inferred from chloroplast DNA sequences (rbcL, matk) and from genomic
RT fingerprinting (ISSR).";

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RL Taxon 52:193-207(2003).
DR EMBL; AJ511370; CAD54514.1; -.
DR GO; GO:0008380; P:RNA splicing; IEA.
DR InterPro; IPR008998; Agglutinin.
DR InterPro; IPR000442; Intron_mature2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_mature2; 1.
DR Pfam; PF01824; MatK_N; 1.
DR PIRam; PIR002866; MatK_N.
SQ SEQUENCE 521 AA; 62784 MW; 58B661FF1185922E CRC64;

Query Match
Best Local Similarity 87.8%; Score 36; DB 2; Length 521;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLR 7
   |||||
Db 235 KOSYNLR 241

RESULT 15
Q6NSV1 PRELIMINARY; PRT; 186 AA.
ID Q6NSV1
AC Q6NSV1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Possible flavin-dependent oxidoreductase.
GN OrderedLocNames=RP2869;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Lattner F.W., Chain B., Hauser L., Lamerdin J.E., Majfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Harrison F.H., Gibson J.E., Bobst C., Torres y Torres J.L., Peters C.,
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572602; CAE28310.1; -.
DR InterPro; IPR005025; FMN_red.
DR Pfam; PF03358; FMN_red; 1.
KW Complete proteome.
SQ SEQUENCE 186 AA; 20152 MW; E7D868C8DD44064E CRC64;

Query Match
Best Local Similarity 80.5%; Score 33; DB 2; Length 186;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOSYNLR 8
   ||:|:|
Db 16 KOSYNLR 23

Search completed: March 1, 2005, 17:43:20
Job time : 52.8154 secs

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